

EAST COAST FEVER VACCINE BASED ON CTL-SPECIFIC SCHIZONT ANTIGENS

BACKGROUND INFORMATION

Theilerioses are a group of disease syndromes affecting cattle, sheep, goats and domestic buffalo caused by tick-borne haemo-protozoan parasites in the genus *Theileria*. The most economically important diseases include Mediterranean fever, East Coast fever (ECF) and malignant theileriosis. Mediterranean fever caused by *Theileria annulata* occurs in North Africa, southern Europe, Near East, Middle East and many parts of Far East Asia with a population of 200 million cattle and buffalo at risk. ECF, caused by *T. parva*, affects 30 million cattle in eastern, central and southern Africa. Malignant theileriosis caused by *T. lestoquardi* affects sheep and goats in southeastern Europe, North Africa, the Near and Middle East and southern Russia and neighbouring States. These parasites belong to the same api-complex group as *Plasmodium falciparum*, *Toxoplasma gondii*, *Cytosauzoon spp*, *Eimeria spp* and *Babesia spp*, with a life-cycle having the arthropod and mammalian components in which sexual and asexual stages develop, respectively. The pathogenic stages of *Theileria* parasites differ. *T. parva* causes a lympho-proliferative disorder in which schizont-infected lymphoblasts are responsible for the pathogenesis of the disease. On the other hand, anaemic disease caused by *T. lestoquardi* and *T. sergenti* is due to piroplasm-infected erythrocytes while both the schizont and piroplasm of *T. annulata* are pathogenic resulting in lympho-proliferative and anaemic syndromes, respectively.

Currently, theilerioses are controlled largely by tick control using acaricides and through "infection and treatment" vaccination protocols, of animals at risk. Such vaccination protocols are deemed effective in that an animal vaccinated in this manner will not develop ECF disease upon exposure to infectious *T. parva*. Due to cost and problems of tick resistance and environmental pollution, control of these diseases through acaricidal destruction of ticks is not sustainable. Vaccination, on the other hand, while effective, presents with certain shortcomings associated with the use of live vaccines. Owing to the ease of transmission of *T. annulata*, infected blood was originally used to immunise cattle by employing parasites of low virulence as the immunizing agent. However, such immunisations were still accompanied by clinically-detectable infection episodes. With the advent of *in vitro* cultivation of *T. annulata* (Sharma et al., 1998) and the development of bulk culture techniques in the 1960s, significant progress was made in realising a more practical immunisation strategy. Currently, passage-attenuated cultures of *T. annulata* are routinely used in national vaccination programs in affected countries. By contrast, similar efforts

to immunise cattle against *T. parva* have been unsuccessful. This is attributed to the failure of attenuated *T. parva* parasites to induce immunity. In addition, much higher numbers of *T. parva*-infected cells are required to infect cattle reliably, since the schizonts of *T. parva* transfer at a low frequency and donor cells get rejected before successful transfer. *T. lestoquardi* has also been cultivated *in vitro* and studies have shown that attenuated parasites can be used to immunise animals with a degree of success.

Given the unsuccessful attempts to immunise cattle with attenuated *T. parva*, subsequent efforts have focused on the use of virulent parasites with accompanying chemotherapy. The rationale of this infection and treatment method (ITM) is to allow the infection to establish and suppress development of frank clinical disease by administering theileriacidal drugs. Animals thus immunised were found to be protected against the development of disease when exposed to the homologous parasite. This vaccination strategy has undergone successive refinements including the use of cryopreserved triturated tick stabilites containing sporozoites (the parasite stage infective for cattle lymphocytes) to standardise the immunisation-infection dose, as well as simultaneous drug administration. Further improvement of this immunisation approach has involved the identification and use of a combination of parasite stocks to broaden the immunising spectrum of the vaccine against several field *T. parva* parasite populations. The use of local parasite stocks to immunise in areas where they have been isolated is also practised. ITM immunisation against *T. parva* has been tested extensively under laboratory and field conditions and is now deployed in the affected region to control ECF.

ITM has a number of practical limitations that hinder its application as a sustainable control measure against ECF in those geographical areas most affected by the disease. Being live, it requires a cold refrigerator chain, which is impractical in Africa. ITM can also cause clinical disease if drug application is inadequate and it has the potential to introduce new parasite strains in areas under the vaccination campaign. The cost (US\$10-20 per immunisation) of this current vaccine is well beyond the budget of poor farmers with cattle afflicted by ECF, due to both the cost of the drugs and the requirement for a trained veterinarian to administer the vaccine. Because of these concerns associated with the ITM vaccine protocol, a great deal of investment has been put in research work to develop a vaccine that will be sustainable and affordable.

Antigens of many parasitic protozoans that induce a protective antibody response against the development of disease have been identified. For example, the major merozoite surface protein of *Plasmodium* species has been shown to be a target of varying degrees of protective

immunity against the asexual blood stages in rodent and human malaria. Vaccination of mice with purified P230, the major merozoite surface protein of the rodent malaria *Plasmodium yoelii*, has resulted in reduced parasitemias in comparison to controls upon intravenous challenge with a lethal dose of parasitized erythrocytes (Holder et al. 1981. Nature 294:361). Mice have also been
5 protected against *P. yoelii* by passive transfer of a monoclonal antibody (Mab) specific for P230 (Majarian et al. 1984. J. Immunol. 132:3131). Mice have also been immunized against (rodent malaria) *Plasmodium chabaudi adami* challenge, by passive immunization with a monoclonal antibody specific for the homologous 250-kDa molecule of this *Plasmodium* species (Lew et al. 1989. Proc. Natl. Acad. Sci. USA 86:3768).

10 A 67 kDa glycoprotein (p67) from the surface of the *T. parva* sporozoite has been isolated (U.S. Patent Number 5273744) and used in a variety of immunization protocols, with little success reported so far, in the development of practical levels of immune-mediated disease resistance. However, cattle recovering from a single infection with *T. parva* sporozoites resist infection upon homologous challenge. Such animals have weak antibody and T cell responses to
15 p67. There is a need to identify *T. parva* antigens that can induce antigen-specific class I MHC-restricted CD8⁺ cytotoxic T lymphocytes (CTLs).

SUMMARY OF THE INVENTION

The present invention relates, e.g., to methods for the identification of parasite antigens,
20 such as *Theileria parva* antigens, that trigger antigen-specific cytotoxic T lymphocyte (CTLs) responses, for inducing immunoprotection against *T. parva* in bovine species and compositions identified by this method that can be used to generate a protective response in cattle, to resist the development of ECF disease, when challenged with infectious *T. parva* material. More particularly, the method includes steps wherein the stimulation of responding lymphocytes to cells
25 transfected by cDNAs encoding parasite antigen is measured in a high throughput manner, by the release of soluble factors, such as gamma interferon, using either an antibody-elispot assay or a bioassay employing endothelial cells. The use of immortalized skin fibroblast cells from outbred animals that have recovered from exposure, as antigen presenting cells, enables the antigen identification, especially where cloned bovine MHC class I genes are not available for co-
30 transfection into COS cells. In addition, high throughput protocols have been developed that allow the resolution of the identity of individual antigens from candidate cDNA pools. Candidate antigens and epitopes, and the nucleotide sequences that encode or result in the production of

these candidate antigens and/or epitopes, identified using these method steps, can be used to stimulate CTLs and to successfully immunize cattle against infection with subsequent exposure to *T. parva* expressing such antigens.

One aspect of the invention is an isolated polypeptide, comprising a sequence
5 represented by one of SEQ ID NO:1 through SEQ ID NO:7; SEQ ID NO:9; or SEQ ID NO: 14 through SEQ ID NO:17. Such isolated polypeptides are sometimes referred to herein as "polypeptides of the invention." In embodiments, an isolated polypeptide of the invention is in detectable amounts in isolates of *T. parva*; and/or comprises a *T. parva* antigen.

Another aspect of the invention is a pharmaceutical composition, which comprises one or
10 more polypeptides of the invention and a pharmaceutically acceptable carrier or excipient.

Another aspect of the invention is an immunogenic composition, which comprises one or more polypeptides of the invention and, optionally, an adjuvant. The immunogenic composition may stimulate cytotoxic T cells specific to the polypeptide; and/or comprise an epitope that stimulates *Theileria parva* (*T. parva*)- specific cytotoxic T cells. Another aspect of the invention is a vaccine,
15 which comprises one or more polypeptides of the invention and, optionally, an adjuvant. In an embodiment of the invention, the vaccine protects an animal against *T. parva* infection.

Another aspect of the invention is an isolated polynucleotide comprising:

- (a) a sequence represented by one of SEQ ID NO:18 through SEQ ID NO: 23 or SEQ ID NO: 28 through SEQ ID NO:31;
- 20 (b) a sequence which is at least about 90% identical to a sequence of (a);
- (c) a sequence which hybridizes under conditions of high stringency to a polynucleotide which comprises a sequence of (a);
- (d) a sequence which encodes a polypeptide represented by SEQ ID NO:1 through SEQ ID NO:7; SEQ ID NO:9; or SEQ ID NO: 14 through SEQ ID NO:17; or
- 25 (e) a complement of any of (a), (b), (c) or (d). Such isolated polynucleotides are sometimes referred to herein as "polynucleotides of the invention."

Other aspects of the invention include a pharmaceutical composition comprising a polynucleotide of the invention and a pharmaceutically acceptable carrier or excipient; a recombinant construct comprising a polynucleotide of the invention, which is operably linked to an
30 expression control sequence; and a vector comprising such a construct. A vector of the invention may further comprise one or more sequences encoding a selectable marker; and the vector may comprise a plasmid, a bacteriophage, a minichromosome or a eukaryotic virus vector. Another

aspect of the invention is a host cell (e.g., a prokaryotic cell or a eukaryotic cell) which comprises a polynucleotide or a vector of the invention. Another aspect of the invention is a method for producing a polypeptide which stimulates a *T. parva*-antigen specific cytotoxic lymphocyte (CTL), comprising culturing a host cell of the invention under conditions effective for producing a
5 polypeptide encoded by the polynucleotide, and harvesting the polypeptide.

Another aspect of the invention is an antibody (e.g., a polyclonal antibody or a monoclonal antibody) specific for a polypeptide of the invention. In an embodiment of the invention, the antibody is coupled to a carrier and/or a label.

Another aspect of the invention is a method for preparing a polyclonal antibody,
10 comprising immunizing an animal with one or more polypeptides of the invention, or with cells comprising polynucleotides or vectors of the invention. Another aspect of the invention is a method for preparing a monoclonal antibody, comprising (a) immunizing an animal with a polypeptide of the invention; (b) recovering cells from the animal which produce antibody that binds to the polypeptide; (c) preparing a hybridoma with the cells isolated in (b), and (d)
15 recovering a monoclonal antibody from the hybridoma that binds to the polypeptide in (a).

Another aspect of the invention is a method for preparing a monoclonal antibody, comprising: (a) immunizing an animal with a host cell comprising a polynucleotide or vector of the invention; (b) recovering cells from the animal which produce antibody that binds to a polypeptide produced by the host cell; (c) preparing hybridomas with the cells isolated in (b), and (d) recovering a
20 monoclonal antibody from the hybridoma that binds to the polypeptide in (b).

Another aspect of the invention is a kit for detecting the presence of *T. parva* in a sample suspected of containing *T. parva*, or for purifying *T. parva* from a sample containing *T. parva*, comprising an antibody of the invention. The kit may further comprise means for performing an enzyme-linked or Western blot assay to detect the presence of *T. parva*; and/or means for binding
25 the antibody to *T. parva* in the sample, and for releasing the organism from the antibody.

Another aspect of the invention is a method for protecting an animal against infection by *T. parva*, comprising administering to the animal a polypeptide of the invention, under conditions effective for the animal to generate a protective antibody against the polypeptide, or effective for the animal to generate *T. parva*-antigen-specific CTLs. Another aspect of the invention is a
30 method for protecting an animal against infection by *T. parva*, comprising administering to the animal a cell comprising a polynucleotide or vector of the invention, under conditions effective for the animal to generate a protective antibody against a polypeptide encoded by the polynucleotide

(expressed from the polynucleotide), or effective for the animal to generate *T. parva*-antigen-specific CD4+ helper and CD8+ CTL responses.

Another aspect of the invention is a method for detecting a pathogenic protozoan infection in a subject, comprising contacting peripheral blood monocytes from the subject with
5 peptide-antigen pulsed cytotoxic T lymphocytes, wherein the cytotoxic T lymphocytes are obtained from an animal to which has been administered a polypeptide of the invention, under conditions effective for the animal to generate *T. parva*-antigen-specific CTLs, or effective for the animal to generate *T. parva*-antigen-specific CD4+ helper and CD8+ cytotoxic T lymphocyte responses. Another aspect of the invention is a method for detecting *T. parva* in a sample suspected
10 of containing *T. parva*, comprising detecting in the sample a polynucleotide of the invention. Any of the methods of the invention, including these detection methods, may be high throughput methods.

Another aspect of the invention is a method for identifying *T. parva* in a sample suspected of containing *T. parva*, comprising contacting the sample with an antibody of the
15 invention, under conditions effective for the antibody to bind specifically to its cognate antigen, and detecting the presence of bound antibody. In embodiments of the invention, the detection is carried out by enzyme immunoassay, radioimmunoassay, fluorescence immunoassay, flocculation, particle agglutination, flow microfluorimetry, a competition assay, or *in situ* chromogenic assay; the antibody is either a monoclonal antibody or a polyclonal antibody; the assay is quantitative; or
20 the assay is high throughput.

Another aspect of the invention is a method for the identification of parasite antigens that are targets of cytotoxic T lymphocytes, comprising co-culturing immortalized fibroblast cell lines transfected with pooled cDNA harvested from a pathogen, with clones of lines of cytotoxic T cells, generated in an animal that has been immunized, by infection and treatment with the pathogen and
25 assaying the supernatant from the co-culture for the presence of a soluble factor. In embodiments of this method, the soluble factor is a cytokine, *e.g.* a gamma interferon; the pathogen is a protozoan organism (*e.g.* an organism in the genus *Theileria*, such as *T. parva*); the fibroblast cell line is of bovine origin; or the fibroblast cell line of bovine origin displays bovine Class I, MHC antigens. The method may further comprise assaying the supernatant of co-cultured cells, for the
30 presence of a soluble factor, secreted by the cytotoxic T cells.

Another aspect of the invention is a method for a multi-matrix (e.g., a three-way matrix) resolution for identification of a single cDNA clone from a pool of cDNAs, in high throughput procedures, comprising:

- (a) preparing a culture of transformed cells by transforming bacterial cells with DNA from a pool of about 25 to about 500 cDNAs, wherein said pool has tested positive in a routine assay;
- (b) diluting the culture of transformed cells so as to yield a density of about 500-5000 growth colonies per 150 cm², when plated on agar-containing plates;
- (c) picking about 100 to 500 colonies from the growth cultures;
- (d) placing about 5 to 60 pools of about 10-100 individual cultures grown from the colonies, into numbered tubes, in such a manner such that each individual bacterial culture is present in more than one of said pools, so that tubes are labeled with a unique number and positioned so that a matrix of tubes is created so as to accommodate a multi-channel pipetting device;
- (e) creating a corresponding matrix table by arraying the numbers on the corresponding tubes containing the pools into a matrix table;
- (f) testing the DNA from each of the tubes in a screening assay; and
- (g) identifying the individual positive colony by comparing the results with the matrix array.

In embodiments of this three way matrix resolution method, the screening assay causes the release of gamma interferon by CD8⁺ cytotoxic T cells; or the soluble factor is a cytokine, e.g. gamma interferon. The method may further comprise assaying the supernatant of co-cultured cells, for the presence of a soluble factor, secreted by the cytotoxic T cells.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a photograph of an autoradiograph of ³²P-labelled double stranded cDNA copied from the poly(A⁺) *T. parva*, schizont RNA, used as starting material for the production of a cDNA expression library of *T. parva*, schizont stage material. The autoradiograph of electrophoresis gel of the 4 fractions (A, B, C and D) of ³²P-labelled ds-cDNA indicates the cDNA sizes in kilobases.

FIG. 2 is a graph, indicating positive cDNA pools, for expression of cloned *T. parva* antigens as measured by the Elispot technique where schizont cDNA pools, were co-cultured with cytotoxic T lymphocyte cell (CTL) lines, and then CTL gamma interferon secretion levels were

used to identify those clones that elicited antigen-specific stimulation. Screening of schizont cDNA pools (B series) was performed with BV115 (4229 TpM) CD8 polyclonal CTL. COS-7 cells co-transfected with BoLA class I HD6 cDNA and schizont cDNA pools were cultured with CTL and recognition assessed by IFN- γ ELISpot. Responses are presented as mean spot forming cell (SFC)/well. Of the 200 cDNA pools tested, pools B42 and B162 were selected as putative positives and subjected to resolution.

FIG. 3 is a graph of Elispot data, indicating the mean spot forming cells/well when COS-7 cells, co-transfected with a bovine MHC Class I gene and *T. parva* schizont cDNAs consisting of a pool of 10 cDNAs, were co-cultured with cytotoxic T lymphocyte cell (CTL) lines, as measured by CTL gamma interferon secretion, in a matrix comparison to reveal nucleotides encoding CTL-stimulating antigens. In this screening of resolved schizont cDNA pool B162 with BV115 (4229 TpM) CD8 polyclonal CTL. 48 pools of 10 cDNA derived were constructed in a 3 way matrix and co-transfected with HD6 into COS-7 cells. Recognition of transfectants by CTL was assessed by IFN- γ ELISpot. IFN- γ production is presented as mean number of spot forming cell (SFC)/well. Of the 48 cDNA pools, 8 were positive, the 3 way matrix was then decoded to reveal 5 single cDNA.

FIG. 4 is a graph that indicates individual single *T. parva* schizont cDNA clones, expressing stimulatory antigen. This screening of single schizont cDNA with BV115 (4229 TpM) CD8 polyclonal CTL following resolution of schizont cDNA pool B162. Five single cDNA decoded from the 3 way matrix were co-transfected with HD6 into COS-7 cells. Recognition of transfectants by CTL was assessed by IFN- γ ELISpot. IFN- γ production is presented as mean number of spot forming cells (SFC)/well. Of the 5 single cDNA, 3 were positive, the 3 had identical sequences and were different from the 2 negative cDNA.

FIG. 5 is a graph of Elispot data, indicating the mean spot forming cells/well when COS-7 cells, co-transfected with a bovine MHC Class I gene and an individual single *T. parva* schizont cDNA clone, Tp1, were co-cultured with cytotoxic T lymphocyte cell (CTL) lines, as measured by CTL gamma interferon secretion. Confirmation of BoLA class I HD6 restriction of Tp1 recognition. Tp1 cDNA was co-transfected into COS-7 cells with BoLA class I HD6 cDNA, BoLA class I KN104 cDNA or alone. Recognition of transfectants by BV115 (4229 TpM) CD8+ polyclonal CTL was assessed by IFN- γ ELISpot. IFN- γ production is presented as mean number of spot forming cells (SFC)/well. Only when Tp1 was co-transfected with HD6 cDNA did the CTL respond.

FIG. 6 is a graph of Elispot data comparing the ability of COS-7 co-transfected cells to present target antigen to CTLs, to the ability of immortalized skin fibroblast cells (iSF) to present target antigen to CTLs. Comparison of ability COS-7 and iSF to present target antigen containing schizont cDNA pools to CTL. COS-7 were co-transfected with HD6 cDNA and schizont cDNA pools, whilst BV115 iSF were transfected with the schizont cDNA pools alone. Recognition of transfectants by BV115 (4229) CD8+ polyclonal CTL was assessed by IFN- γ ELISpot. IFN- γ production is presented as mean number of spot forming cells (SFC)/well. Of the 7 pools tested only one, pool B42, gave a response above that of the untransfected cells. This pool was known to contain the Tp1 cDNA. The weaker response to transfected iSF is likely due to an inferior transfection efficiency compared to COS-7.

FIG. 7A is a graph of Elispot data (gamma interferon production); FIG. 7B is a graph of bioassay data (MHC Class II expression), for Tp1 transfected COS-7 cells. Both assays show the need for co-transfection of COS-7 cells with HD6 (MHC Class I) cDNA for the CTLs to be stimulated by Tp1 production. Comparison of detection of CTL IFN- γ release by ELISpot (A) and Bioassay (B) following recognition of Tp1 transfected COS-7 cells.

Single cDNA isolated following resolution of positive cDNA pool B42 were transfected into COS-7 cells with or without HD6 cDNA. Recognition of transfectants by BV115 (4229) CD8+ polyclonal CTL was assessed by release of IFN- γ using both an ELISpot and bioassay. IFN- γ production as detected by ELISpot is presented as mean number of spot forming cells (SFC)/well and IFN- γ bioactivity presented as % MHC class II expression. Of the 9 cDNA tested, both assays showed HD6 dependent recognition of 3 (#4, 178 and 309). All cDNA were sequenced and the positive cDNA identified as Tp1.

FIG. 8 is a graph of data that indicates the % lysis of COS-7 cells, co-transfected with a MHC Class I gene and a cDNA for Tp1 by CTLs. Note that lysis was abrogated when an anti-BoLA class I monoclonal antibody ("MHC I-block") was used to mask MHC Class I expression. Lysis of Tp1 transfected COS-7 cells (co-transfection with BoLA class I HD6 cDNA) and immortalised autologous skin fibroblasts (SF) by the schizont specific BV115 (4229 TpM) CD8+ polyclonal CTL line. HD6 expressing 4229 TpM line was included as a positive control and PIM transfected COS-7 cells and iSF included as negative controls. MHC class I restriction was assessed by pre-incubating Tp1 transfected COS cells with an anti-BoLA class I mAb (MHC I block).

FIG. 9 indicates the deduced amino acid sequence of Exonuclease III-deleted, Tp1 cDNA plasmids (SEQ ID NOS 1, 6, 7 & 43-46, respectively, in order of appearance). Clones were co-transfected with HD6 cDNA and recognition by CTL determined by IFN- γ ELISpot. Only the Tp1 orf and clones Tp1 Del1 and Del2 were recognised implying that the HD6 restricted Tp1 epitope lay between amino acid position 141 and 241.

FIG. 10 indicates the deduced amino acid sequence of a series of deleted Tp1 clones (SEQ ID NOS 47-52, respectively, in order of appearance). The small m in bold represents the methionine added by the artificial ATG start codon by PCR. Constructs were co-transfected with HD6 cDNA and recognition by CTL determined by IFN- γ ELISpot. Clones Tp1.1, 1.4 and 1.6 were recognised by CTL thus narrowing down the epitope containing region to 66 amino acids.

FIG. 11 is a graph of Elispot data indicating mapping of a Tp1 epitope using a synthetic peptide library. This figure shows the fine mapping of the HD6 restricted Tp1 CTL epitope using synthetic peptide library. Twenty eight 12mer peptides overlapping by two amino acids encompassing the 66 amino acids encoded by the Tp1.2 insert were synthesised and used at a final concentration of 1 μ g/ml to pulse BV115 iSF. Recognition of peptide pulsed iSF by two polyclonal CTL lines derived from BV115, one maintained on 4229 TpM (4229 poly) the other on autologous BV115 TpM (BV115 poly), was assessed by IFN- γ ELISpot. Significant responses were observed against peptides #10 and 11 that corresponded to the amino acid sequence RCVGYPKVKEEMLE (SEQ ID NO: 8).

FIG. 12 is a graph of Elispot data indicating mapping of the minimal length of the HD6 restricted epitope of Tp1 by the identification of the HD6 restricted Tp1 CTL epitope using synthetic peptides. Twenty seven peptides comprising of all the possible 9, 10 and 11mers from the sequence FLVGYPKVKEEMLEMA (SEQ ID NO: 32) were synthesised and used at a final concentration of 100pg/ml to pulse P815 cells stably expressing HD6 (P815/HD6). Recognition of peptide pulsed P815/HD6 by two HD6 restricted BV115 CTL clones, #94 and #122, was assessed by IFN- γ ELISpot. Significant responses were only observed against peptide #24, suggesting that the HD6 was the 11mer VGYPKVKEEML (SEQ ID NO: 9).

FIG. 13 is a comparison of the deduced amino acid sequences of Tp1 from two different *T. parva* strains, Muguga (SEQ ID NO: 1) and Marikebuni SEQ ID NO: 53). There was 95.8% identity in 542 aa overlap. Significantly there were two amino acid differences at positions 226 and 227, the C terminal end of the 11 amino acid HD6 restricted epitope.

FIG.14 is a graph of Elispot data that indicates the response of CD8+ T cells, harvested from an immune bull to the HD6 restricted epitope of Tp1. Measurement of the Tp1 specific CD8+ T cell responses of an immune bull following challenge with *T. parva* sporozoites are indicated. CD8+ T cells were purified from peripheral blood at various time-points and incubated with the HD6 restricted Tp1 11mer synthetic (epitope) or a Tp1 peptide which had not previously been shown to contain a CTL epitope (control) and responses were measured by IFN-Gamma ELISpot assay.

FIG. 15A is a photograph of a Coomassie stained gel and an anti-His-tag immunoblot (Western blot) of Tp1 expression, using a bacterial expression vector; FIG. 15B is a photograph of a Coomassie stained gel and an anti-His-tag immunoblot of Tp4 expression, using a bacterial expression vector; and, FIG. 15C is a photograph of a Coomassie stained gel and an anti-His-tag immunoblot of Tp5 expression, using a bacterial expression vector. The expression of CTL target antigens, Tp1 (A), Tp4 (B) and Tp5 (C) proteins was investigated. Recombinant proteins were isolated by Ni-NTA agarose and run on 12% SDS-PAGE gels followed by staining using coomassie blue or detection by Western blotting.

FIG.16A is a panel of histograms indicating numbers of infected Bovine lymphocytes, stained with the reporter molecules: control (a); mouse polyclonal antibody to Tp1 (b); mouse monoclonal antibody to Tp1 (c); mouse polyclonal antibody to Tp4 (d); and mouse polyclonal antibody to Tp5, (e. Monoclonal and polyclonal antibodies raised against the Tp1, Tp4 and Tp5 proteins were used for staining of *T. parva* infected cells. FIG. 16B shows a quantitation of the values shown in the histograms in FIG 16A.

FIG. 17. indicates Tp1 multiple sequence alignments (SEQ ID NOS 54-77, respectively, in order of appearance). Amino acid sequence comparison of a portion (containing the HD6 CTL epitope) of Tp1 generated from *T. parva* isolates from different regions. Domains with variations are underlined.

FIG. 18 indicates the level of CTL responses to several Tp antigens, following CP(Canary Pox mediated)/MVA (modified Vaccinia Virus Ankara-vector mediated) immunization protocols. The data indicates the production of *T. parva* antigen-specific CD8 (CTLs) in animals following immunization protocols with CanaryPox viral vectors, expressing *T. parva* antigen.

FIG. 19 indicates the level of CTL responses to several Tp antigens, following DNA/MVA immunization protocols. The data indicates the production of *T. parva* antigen-

specific CD8 (CTLs) in animals following immunization protocols with modified Vaccinia (Ankara) viral vectors, expressing *T. parva* antigen.

FIG. 20 indicates control data for CP/MVA and DNA/MVA immunization protocols, where cattle were given phosphate buffered saline injections rather than Tp antigens. The control experimental data for measuring the development of CTLs following immunization indicates a lack of *T parva*, antigen-specific CD8+ cells in PBS immunized animals.

DETAILED DESCRIPTION OF THE INVENTION

Class I MHC-restricted CD8⁺ cytotoxic T lymphocytes (CTLs) are responsible for protecting cattle against a lethal challenge with *Theileria parva* (*T. parva*), sporozoites (Morrison, Taracha, and McKeever, 1995). These CTLs are directed at schizont-infected cells, which they recognize and lyse. Schizont antigens that are recognized by these CD8⁺ CTLs are the prime candidates for inclusion into an effective sub-unit vaccine for the prevention of East Coast Fever disease (ECF).

The Examples herein show the identification of a variety of antigens which are suitable for use in subunit vaccines.

The present invention provides polynucleotides, and novel methods for their identification, which encode proteins and peptides that are targets of antigen-specific cytotoxic CD8⁺ T lymphocytes which have been shown to be protective against ECF infection in adoptive cell transfer experiments. Experimental immunisation of cattle with these antigens or recombinant viral vector cell systems producing these antigens have stimulated the production of antigen-specific T cell responses in the immunized animals.

The proteins identified by the novel method can also be used to as antigens to stimulate the production of antibodies. Such antibodies are useful for the detection of the presence of a stimulating antigen, in animals tissues and fluids. Presence of such antigen would indicate infection of the animal by organisms producing or bearing, the antigen. For example, in one embodiment of the present invention, infection of animal by *Theileria parva* (*T. parva*) can be detected by antibodies produced as a result of using peptides encoded by polynucleotide sequences as antigens to stimulate the production of such antibodies

In a particularly preferred embodiment of the subject invention, the antigens encoded by polynucleotide sequences, cloned from expressed genes of *T. parva*, are identified by the use of immortalized cloned bovine skin fibroblast cell lines to stimulate the activation of cytotoxic CD8+

T lymphocytes by antigen when stimulation is measured by the release of soluble factors, more specifically gamma interferon. The subject invention also relates to compositions isolated by methods including one or more of these particular steps and the use of these compositions: to stimulate or induce cytotoxic T cells, as diagnostic reagents for the detection of disease, or an
5 immune response, in kits or high throughput "chip" methods for the detection of or expression of, identical or homologous nucleic acids. In another preferred embodiment of the subject invention, the antigens identified by the novel method are useful for immunization of animals for the production of CTLs that recognize *T. parva*.

The present invention identifies a group of polynucleotide sequences that encode *T. parva*
10 antigens useful for a variety of applications.

The nucleic acids of the invention may comprise recombinant nucleic acid. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro or in a cell in culture, in general, by the manipulation of nucleic acid by endonucleases and/or exonucleases and/or polymerases and/or ligases and/or recombinases, to produce a nucleic acid not normally
15 found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids,
20 once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Furthermore, as a result of the degeneracy of the genetic code, a multitude of nucleotide sequences may be produced which are based upon the sequences provided herein and corresponding peptides, polypeptides, or proteins. Some of these nucleotide sequences will bear
25 only minimal homology to the sequences disclosed herein; however the subject invention specifically contemplates each and every possible variation of nucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the nucleotide sequence of naturally occurring peptide, polypeptide, or protein, and all such variations are to be considered as being
30 specifically disclosed herein. Recombinant nucleotide variants are alternate polynucleotides which encode a particular protein. They may be synthesized, for example, by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which

produce specific restriction sites or codon usage-specific mutations, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic host system, respectively.

It is possible to produce the polynucleotides of the subject invention, or portions thereof, entirely by synthetic chemistry. After synthesis, the nucleic acid sequence can be used alone or joined with a preexisting sequence and inserted into one of the many available DNA vectors and their respective host cells using techniques well known in the art. Moreover, synthetic chemistry may be used to introduce specific mutations into the nucleotide sequence. Alternatively, a portion of sequence in which a mutation is desired can be synthesized and recombined with a portion of an existing genomic or recombinant sequence.

Peptides and polypeptides of the invention can also be produced, entirely or in part, by synthetic chemistry, using conventional procedures.

Nucleotide sequences encoding a peptide, polypeptide, or protein may be joined to a variety of other nucleotide sequences by means of well established recombinant DNA techniques (Sambrook J. et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.; or Ausubel F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York City). Useful sequences include an assortment of cloning vectors such as plasmids, cosmids, lambda phage derivatives, phagemids, and the like. Vectors of interest include vectors for replication, expression, probe generation, sequencing, and the like. In general, vectors of interest may contain an origin of replication functional in at least one organism, convenient restriction endonuclease sensitive sites, and selectable markers for one or more host cell systems.

Another aspect of the subject invention is to provide for hybridization probes which are capable of hybridizing with naturally occurring antigen sequences or nucleotide sequences encoding the disclosed peptide, polypeptide, or protein. The stringency of the hybridization conditions will determine whether the probe identifies only the native nucleotide sequence or sequences of closely related molecules. If degenerate nucleotide sequences of the subject invention are used for the detection of related sequences, they should preferably contain at least 50% of the nucleotides of the sequences presented herein.

"Probes" are nucleic acid sequences of variable length, preferably between at least about 10 and as many as about 6,000 nucleotides, depending on use. They are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually

obtained from a natural or recombinant source, are highly specific and much slower to hybridize than oligomers. They may be single- or double-stranded and designed to have specificity in PCR, hybridization membrane-based, or ELISA-like technologies.

Hybridization probes of the subject invention may be derived from the nucleotide
5 sequences of the attached List Sequences and the Sequences provided as SEQ ID NO: 18-22 (see, *e.g.*, Figures 9, 10, and 17), or from surrounding or included genomic sequences comprising untranslated regions such as promoters, enhancers and introns. Such hybridization probes may be labeled with appropriate reporter molecules. Means for producing specific hybridization probes include oligolabelling, nick translation, end-labeling or PCR amplification using a labeled
10 nucleotide. Alternatively, the cDNA sequence may be cloned into a vector for the production of mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3 or SP6 and labelled nucleotides. A number of companies (such as Pharmacia Biotech, Piscataway, N.J.; Promega, Madison, Wis.; US Biochemical Corp, Cleveland, Ohio; etc.) supply commercial
15 kits and protocols for these procedures.

The nucleotide sequences (shown as SEQ ID NO: 18-22) can be used to generate probes for mapping the native genomic sequence. The sequence may be mapped to a particular chromosome or to a specific region of the chromosome using well known techniques. These include in situ hybridization to chromosomal spreads, flow-sorted chromosomal preparations, or
20 artificial chromosome constructions such as yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions or single chromosome cDNA libraries.

In situ hybridization of chromosomal preparations and physical mapping techniques such as linkage analysis using established chromosomal markers are invaluable in extending genetic maps in organisms, including intracellular parasites. The nucleotide sequences of the subject
25 invention may also be used to detect differences in the chromosomal location of nucleotide sequences due to translocation, inversion, or recombination.

Other aspects of the invention include use of the disclosed sequences or recombinant nucleic acids derived therefrom to produce purified peptides. The nucleotide sequences as disclosed herein may be used to produce an amino acid sequence using well known methods of
30 recombinant DNA technology. Goeddel (Gene Expression Technology, Methods and Enzymology [1990] Vol 185, Academic Press, San Diego, Calif.) is one among many publications which teach expression of an isolated, purified nucleotide sequence. The amino acid or peptide may be

expressed in a variety of host cells; either prokaryotic or eukaryotic. Some expression vectors are viral vectors such as vaccinia-based vectors and adeno-associated viral vectors, among others (Dunachie and Hill, 2003). Host cells may be from the same species from which the nucleotide sequence was derived or from a different species.

5 Still further aspects of the invention use these purified peptides to produce antibodies or other molecules able to bind to the peptides. These antibodies or binding agents can then be used for the screening of cells in order to localize the cellular distribution of the peptides or proteins. The antibodies are also useful for the affinity purification of recombinantly produced peptides or proteins. Such antibodies are also useful as diagnostic reagents for the detection of protozoan
10 diseases or in antibody-mediated tests and assays.

Disclosed *T. parva* antigens can also be used as a diagnostic aid or in methods that measure the presence of *T. parva* cytotoxic lymphocytes in immunized or infected animals by co-culturing mononuclear cells harvested from an animal suspected to have an infection due to *T. parva*, with a *T. parva* antigen-specific cytotoxic T cell under standard culture conditions for
15 mammalian cell cultures. Mononuclear cells would have been incubated in a culture medium containing an indicator that is released upon cell death, such as ^{51}Cr . This is a method that is well-known in the art.

The disclosed nucleotide sequences can be used individually, or in panels, in tests or assays to detect levels of peptide, polypeptide, or protein expression. The form of such qualitative
20 or quantitative methods may include northern analysis, dot blot or other membrane based technologies, dip stick, pin or chip technologies, PCR, ELISAs or other multiple sample format technologies.

An "oligonucleotide" or "oligomer" is a stretch of nucleotide residues which has a sufficient number of bases to be used in a polymerase chain reaction (PCR). These short
25 sequences are based on (or designed from) genomic or cDNA sequences and are used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides or oligomers comprise portions of a DNA sequence having at least about 10 nucleotides and as many as about 50 nucleotides, preferably about 15 to 30 nucleotides. They can be chemically synthesized and may be used as probes.

30 A "complementary" DNA or RNA is a sequence that is 100% identical to the strand to which it is complementary.

The polynucleotides of the subject invention can themselves be used as probes.

Additional polynucleotide sequences can be added to the ends of (or internally in) the exemplified polynucleotide sequences so that polynucleotides that are longer than the exemplified polynucleotides can also be used as probes. Thus, isolated polynucleotides comprising one or
5 more of the exemplified sequences are within the scope of the subject invention. Polynucleotides that have less nucleotides than the exemplified polynucleotides can also be used and are contemplated within the scope of the present invention. For example, for some purposes, it might be useful to use a conserved sequence from an exemplified polynucleotide wherein the conserved sequence comprises a portion of an exemplified sequence. Thus, polynucleotides of the subject
10 invention can be used to find additional, homologous (wholly or partially) genes.

Probes of the subject invention may be composed of DNA, RNA, or PNA (peptide nucleic acid). The probe will normally have at least about 10 bases, more usually at least about 17 bases, and may have up to about 100 bases or more. Longer probes can readily be utilized, and such probes can be, for example, several kilobases in length. The probe sequence is designed to be
15 at least substantially complementary to a portion of a gene encoding a protein of interest. The probe need not have perfect complementarity to the sequence to which it hybridizes. The probes may be labeled utilizing techniques that are well known to those skilled in this art.

One approach for the use of the subject invention as probes entails first identifying DNA segments that are homologous with the disclosed nucleotide sequences using, for example,
20 Southern blot analysis of a gene bank. Thus, it is possible, without the aid of biological analysis, to know in advance the probable activity of many new polynucleotides, and of the individual gene products expressed by a given polynucleotide. Such an analysis provides a rapid method for identifying commercially valuable compositions.

One hybridization procedure useful according to the subject invention typically includes
25 the initial steps of isolating the DNA sample of interest and purifying it chemically. Either lysed cells or total fractionated nucleic acid isolated from cells can be used. Cells can be treated using known techniques to liberate their DNA (and/or RNA). The DNA sample can be cut into pieces with an appropriate restriction enzyme. The pieces can be interest can be through electrophoresis in a gel, usually agarose or acrylamide. The pieces of interest can be transferred to an
30 immobilizing membrane.

The particular hybridization technique is not essential to the subject invention. As improvements are made in hybridization techniques, they can be readily applied.

The probe and sample can then be combined in a hybridization buffer solution and held at an appropriate temperature until annealing occurs. Thereafter, the membrane is washed free of extraneous materials, leaving the sample and bound probe molecules typically detected and quantified by autoradiography and/or liquid scintillation counting. As is well known in the art, if the probe molecule and nucleic acid sample hybridize by forming a strong non-covalent bond between the two molecules, it can be reasonably assumed that the probe and sample are essentially identical or very similar. The probe's detectable label provides a means for determining in a known manner whether hybridization has occurred.

In the use of the nucleotide segments as probes, the particular probe is labeled with any suitable label known to those skilled in the art, including radioactive and non-radioactive labels. Typical radioactive labels include ^{32}P , ^{35}S , or the like. Non-radioactive labels include, for example, ligands such as biotin or thyroxine, as well as enzymes such as hydrolases or peroxidases, or the various chemiluminescers such as luciferin, or fluorescent compounds like fluorescein and its derivatives. In addition, the probes can be made inherently fluorescent as described in International Application No. WO 93/16094.

Various degrees of stringency of hybridization can be employed. The more stringent the conditions, the greater the complementarity that is required for duplex formation. Stringency can be controlled by temperature, probe concentration, probe length, ionic strength, time, and the like. Preferably, hybridization is conducted under moderate to high stringency conditions by techniques well known in the art, as described, for example, in Keller, G. H., M. M. Manak (1987) DNA Probes, Stockton Press, New York, N.Y., pp. 169-170.

As used herein "moderate to high stringency" conditions for hybridization refers to conditions that achieve the same, or about the same, degree of specificity of hybridization as the conditions described herein. Examples of moderate to high stringency conditions are provided herein. Specifically, hybridization of immobilized DNA on Southern blots with ^{32}P -labeled gene-specific probes is performed using standard methods (Maniatis et al.). In general, hybridization and subsequent washes are carried out under moderate to high stringency conditions that allow for detection of target sequences with homology to sequences exemplified herein. For double-stranded DNA gene probes, hybridization can be carried out overnight at 20-25° C. below the melting temperature (T_m) of the DNA hybrid in 6 x SSPE, 5 x Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. The melting temperature is described by the following formula from Beltz et al. (1983):

$T_m = 81.5^\circ \text{C} + 16.6 \log[\text{Na}^+] + 0.41(\% \text{G+C}) - 0.61(\% \text{formamide}) - 600/\text{length of duplex in base pairs}$.

Washes can typically be carried out as follows:

(1) Twice at room temperature for 15 minutes in 1.times. SSPE, 0.1% SDS (low stringency wash).

(2) Once at $T_m - 20^\circ \text{C}$. for 15 minutes in 0.2.times. SSPE, 0.1% SDS (moderate stringency wash).

For oligonucleotide probes, hybridization was carried out overnight at $10-20^\circ \text{C}$ below the melting temperature (T_m) of the hybrid in 6xSSPE, 5xDenhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. T_m for oligonucleotide probes was determined by the following formula from Suggs et al. (1981):

$$T_m (^\circ \text{C}) = 2(\text{number T/A base pairs}) + 4(\text{number G/C base pairs})$$

In general, salt and/or temperature can be altered to change stringency. With a labeled DNA fragment of greater than about 70 or so bases in length, the following conditions can be used:

Low: 1 or 2X SSPE, room temperature Low: 1 or 2X SSPE, 42°C . Moderate: 0.2X or 1X SSPE, 65°C . High: 0.1X SSPE, 65°C .

Duplex formation and stability depend on substantial complementarity between the two strands of a hybrid, and, as noted above, a certain degree of mismatch can be tolerated. Therefore, polynucleotide sequences of the subject invention include mutations (both single and multiple), deletions, and insertions in the described sequences, and combinations thereof, wherein said mutations, insertions, and deletions permit formation of stable hybrids with a target polynucleotide of interest. Mutations, insertions, and deletions can be produced in a given polynucleotide sequence using standard methods known in the art. Other methods may become known in the future.

The mutational, insertional, and deletional variants of the polypeptide sequences of the invention can be used in the same manner as the exemplified polynucleotide sequences so long as the variants have substantial sequence similarity with the original sequence. As used herein, substantial sequence similarity refers to the extent of nucleotide similarity that is sufficient to enable the variant polynucleotide to function in the same capacity as the original sequence. Preferably, this similarity is greater than 50%; more preferably, this similarity is greater than 75%; and most preferably, this similarity is greater than 90%. The degree of similarity needed for the

variant to function in its intended capacity will depend upon the intended use of the sequence. It is well within the skill of a person trained in this art to make mutational, insertional, and deletional mutations that are designed to improve the function of the sequence or otherwise provide a methodological advantage.

5 PCR technology. Polymerase Chain Reaction (PCR) is a repetitive, enzymatic, primed synthesis of a nucleic acid sequence. This procedure is well known and commonly used by those skilled in this art (see U.S. Pat. Nos. 4,683,195, 4,683,202, and 4,800,159; Saiki et al., 1985). PCR is based on the enzymatic amplification of a DNA fragment of interest that is flanked by two oligonucleotide primers that hybridize to opposite strands of the target sequence. The primers are oriented with the 3' ends pointing towards each other. Repeated cycles of heat denaturation of the template, annealing of the primers to their complementary sequences, and extension of the annealed primers with a DNA polymerase result in the amplification of the segment defined by the 5' ends of the PCR primers. Since the extension product of each primer can serve as a template for the other primer, each cycle essentially doubles the amount of DNA fragment produced in the previous cycle. This results in the exponential accumulation of the specific target fragment, up to several million-fold in a few hours. By using a thermostable DNA polymerase such as Taq polymerase, which is isolated from the thermophilic bacterium *Thermus aquaticus*, the amplification process can be completely automated. Other enzymes that can be used are known to those skilled in the art.

20 The polynucleotide sequences of the subject invention (and portions thereof such as conserved regions and portions that serve to distinguish these sequences from previously-known sequences) can be used as, and/or used in the design of, primers for PCR amplification. In performing PCR amplification, a certain degree of mismatch can be tolerated between primer and template. Therefore, mutations, deletions, and insertions (especially additions of nucleotides to the 5' end) of the exemplified polynucleotides can be used in this manner. Mutations, insertions and deletions can be produced in a given primer by methods known to an ordinarily skilled artisan.

25 Full length genes may be cloned utilizing partial nucleotide sequence and various methods known in the art. Gobinda et al. (1993; PCR Methods Applic 2:318-22) disclose "restriction-site PCR" as a direct method which uses universal primers to retrieve unknown sequence adjacent to a known locus. First, genomic DNA is amplified in the presence of primer to linker and a primer specific to the known region. The amplified sequences are subjected to a second round of PCR with the same linker primer and another specific primer internal to the first

one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR can be used to acquire unknown sequences starting with primers based on a known region (Triglia T. et al. (1988) *Nucleic Acids Res* 16:8186). The method uses several
5 restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template. Divergent primers are designed from the known region. The multiple rounds of restriction enzyme digestions and ligations that are necessary prior to PCR make the procedure slow and expensive (Gobinda et al. [1993] *supra*).

10 Capture PCR (Lagerstrom M. et al. (1991) *PCR Methods Applic* 1:111-19) is a method for PCR amplification of DNA fragments adjacent to a known sequence in eucaryotic and YAC DNA. As noted by Gobinda et al. (1993, *supra*), capture PCR also requires multiple restriction enzyme digestions and ligations to place an engineered double-stranded sequence into an unknown portion of the DNA molecule before PCR. Although the restriction and ligation
15 reactions are carried out simultaneously, the requirements for extension, immobilization and two rounds of PCR and purification prior to sequencing render the method cumbersome and time consuming.

Parker J. D. et al. (*Nucleic Acids Res* [1991] 19:3055-60), teach walking PCR, a method for targeted gene walking which permits retrieval of unknown sequences. PromoterFinder.TM. is
20 a kit available from Clontech Laboratories, Inc. (Palo Alto, Calif.) which uses PCR and primers derived from p53 to walk in genomic DNA. Nested primers and special PromoterFinder.TM. libraries are used to detect upstream sequences such as promoters and regulatory elements. This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

One PCR method replaces methods which use labeled probes to screen plasmid libraries
25 and allow one researcher to process only about 3-5 genes in 14-40 days. In the first step, which can be performed in about two days, any two of a plurality of primers are designed and synthesized based on a known partial sequence. In step 2, which takes about six to eight hours, the sequence is extended by PCR amplification of a selected library. Steps 3 and 4, which take about one day, are purification of the amplified cDNA and its ligation into an appropriate vector. Step 5,
30 which takes about one day, involves transforming and growing up host bacteria. In step 6, which takes approximately five hours, PCR is used to screen bacterial clones for extended sequence. The final steps, which take about one day, involve the preparation and sequencing of selected clones.

If the full length cDNA has not been obtained, the entire procedure is repeated using either the original library or some other preferred library. The preferred library may be one that has been size-selected to include only larger cDNAs or may consist of single or combined commercially available libraries, e.g., from Clontech Laboratories, Inc. (Palo Alto, Calif.). The cDNA library may have been prepared with oligo (dT) or random priming. Random primed libraries are preferred in that they will contain more sequences which contain 5' ends of genes. A randomly primed library may be particularly useful if an oligo (dT) library does not yield a complete gene. It must be noted that the larger and more complex the protein, the less likely it is that the complete gene will be found in a single plasmid.

CLONTECH PCR-Select.TM. cDNA Subtraction (Clontech Laboratories, Inc., Palo Alto, Calif.) is yet another means by which differentially expressed genes may be isolated. The procedure allows for the isolation of transcripts present in one mRNA population which is absent, or found in reduced numbers, in a second population of mRNA. Rare transcripts may be enriched 1000-fold.

Another method for analyzing either the size or the nucleotide sequence of PCR products is capillary electrophoresis. Systems for rapid sequencing are available from Perkin Elmer (Foster City Calif.), Beckman Instruments (Fullerton, Calif.), and other companies. Capillary sequencing employs flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity is converted to electrical signal using appropriate software (eg. Genotyper.TM. and Sequence Navigators.TM. from Perkin Elmer) and the entire process from loading of samples to computer analysis and electronic data display is computer controlled. Capillary electrophoresis provides greater resolution and is many times faster than standard gel based procedures. It is particularly suited to the sequencing of small pieces of DNA which might be present in limited amounts in a particular sample. The reproducible sequencing of up to 350 bp of M13 phage DNA in 30 min has been reported (Ruiz-Martinez M. C. et al. [1993] Anal Chem 65:2851-8).

Polynucleotides of the subject invention can be defined according to several parameters. One characteristic is the biological activity of the protein products as identified herein. The proteins and genes of the subject invention can be further defined by their amino acid and nucleotide sequences. The sequences of the molecules can be defined in terms of homology to certain exemplified sequences as well as in terms of the ability to hybridize with, or be amplified

by, certain exemplified probes and primers. Additional primers and probes can readily be constructed by those skilled in the art such that alternate polynucleotide sequences encoding the same amino acid sequences can be used to identify and/or characterize additional genes. The proteins of the subject invention can also be identified based on their immunoreactivity with
5 certain antibodies.

The polynucleotides and proteins of the subject invention include portions, fragments, variants, and mutants of the full-length sequences as well as fusions and chimerics, so long as the encoded protein retains the characteristic biological activity of the proteins identified herein. As used herein, the terms "variants" or "variations" of genes refer to nucleotide sequences that encode
10 the same proteins or which encode equivalent proteins having equivalent biological activity. As used herein, the term "equivalent proteins" refers to proteins having the same or essentially the same biological activity as the exemplified proteins.

Variations of genes may be readily constructed using standard techniques such as site-directed mutagenesis and other methods of making point mutations and by DNA shuffling, for
15 example. In addition, gene and protein fragments can be made using commercially available exonucleases, endonucleases, and proteases according to standard procedures. For example, enzymes such as Bal31 can be used to systematically cut off nucleotides from the ends of genes. Also, genes that encode fragments may be obtained using a variety of restriction enzymes. Proteases may be used to directly obtain active fragments of these proteins. Of course, molecular
20 techniques for cloning polynucleotides and producing gene constructs of interest are also well known in the art. In vitro evaluation techniques, such as MAXYGEN's "Molecular Breeding" can also be applied to practice the subject invention.

A "selectable marker" is a gene whose expression allows one to identify cells that have been transformed or transfected with a vector containing the marker gene.

25 "Reporter" molecules are chemical moieties used for labeling a nucleic or amino acid sequence. They include, but are not limited to, radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents. Reporter molecules associate with, establish the presence of, and may allow quantification of a particular nucleic or amino acid sequence.

A "portion" or "fragment" of a polynucleotide or nucleic acid comprises all or any part of
30 the nucleotide sequence having fewer nucleotides than about 6 kb, preferably fewer than about 1 kb which can be used as a probe. Such probes may be labeled with reporter molecules using nick translation, Klenow fill-in reaction, PCR or other methods well known in the art. After pretesting

to optimize reaction conditions and to eliminate false positives, nucleic acid probes may be used in Southern, northern or in situ hybridizations to determine whether target DNA or RNA is present in a biological sample, cell type, tissue, organ or organism.

A "polypeptide" comprises a protein, oligopeptide or peptide fragments thereof.

5 A "mutant, variant, or modified polypeptide" means any polypeptide encoded by a nucleotide sequence that has been mutated through insertions, deletions, substitutions, or the like.

"Chimeric" molecules are polynucleotides or polypeptides which are created by combining one or more nucleotide or peptide sequences (or their parts). In the case of nucleotide sequences, such combined sequences may be introduced into an appropriate vector and expressed
10 to give rise to a chimeric polypeptide which may be expected to be different from the native molecule in one or more of the following characteristics: cellular location, distribution, ligand-binding affinities, interchain affinities, degradation/turnover rate, signaling, etc.

"Active" is that state which is capable of being useful or of carrying out some role. It specifically refers to those forms, fragments, or domains of an amino acid sequence which display
15 the biologic and/or immunogenic activity characteristic of the naturally occurring peptide, polypeptide, or protein. For example, the present invention relates to active fragments of polypeptides (*e.g.*, represented by SEQ ID NO: 1-5). Each of these active fragments retains at least one epitope of the larger polypeptide.

"Naturally occurring" refers to a polypeptide produced by cells which have not been
20 genetically engineered or which have been genetically engineered to produce the same sequence as that naturally produced.

"Derivative" refers to those polypeptides which have been chemically modified by such techniques as ubiquitination, labeling, pegylation (derivatization with polyethylene glycol), and chemical insertion or substitution of amino acids such as ornithine which do not normally occur in
25 proteins.

"Recombinant polypeptide variant" refers to any polypeptide which differs from naturally occurring peptide, polypeptide, or protein by amino acid insertions, deletions and/or substitutions.

Amino acid "substitutions" are defined as one for one amino acid replacements. They are
30 conservative in nature when the substituted amino acid has similar structural and/or chemical properties. Examples of conservative replacements are substitution of a leucine with an isoleucine or valine, an aspartate with a glutamate, or a threonine with a serine.

Amino acid "insertions" or "deletions" are changes to or within an amino acid sequence. They typically fall in the range of about 1 to 5 amino acids. The variation allowed in a particular amino acid sequence may be experimentally determined by producing the peptide synthetically or by systematically making insertions, deletions, or substitutions of nucleotides in the sequence
5 using recombinant DNA techniques.

An "oligopeptide" is a short stretch of amino acid residues and may be expressed from an oligonucleotide. Such sequences comprise a stretch of amino acid residues of at least about 5 amino acids and often about 17 or more amino acids, typically at least about 9 to 13 amino acids, and of sufficient length to display biologic and/or immunogenic activity.

10 A "standard" is a quantitative or qualitative measurement for comparison. Preferably, it is based on a statistically appropriate number of samples and is created to use as a basis of comparison when performing diagnostic assays, running clinical trials, or following patient treatment profiles. The samples of a particular standard may be normal or similarly abnormal.

15 An antibody or "specific binding parts" means any fragment of an antibody molecule that will bind antigen or other ligands such as lectins or other molecules. "Specific binding parts" is meant to include, but not be limited to antibody fragments such as Fab fragments, Fab'(2) fragments, Fc region fragments, Complementarity determining regions (CDRs), Fv fragments, single chain Fv (scFv) fragments, and antigen binding site fragments.

20 An "antigen" is a macromolecule that is recognized by antibodies or immune cells and can trigger an immune response. Usually, an antigen is a protein or a polysaccharide, but it can be any type of molecule, even small molecules if coupled to a large carrier.

25 An "antigen specific" cytotoxic T cell is a T lymphocyte that can recognize and kill another cell that is expressing an antigen, usually in conjunction with a type or class of molecules referred to by those familiar with the art, as Major Histocompatibility Complex (MHC) Class I molecules. Such Cytotoxic T cells are also referred to as "CD8⁺" (CD8 positive) or CTLs, by those familiar with the art.

30 An epitope or antigenic determinant is a region or section of an antigen that is approximately the minimal length of antigenic sequence that will elicit an immune response, as measured by the development of an antibody response, the development of T antigen-specific T cells, or other measureable immune cell response. For example, an epitope could be a site on an antigen recognized by antibody.

A T cell "epitope" is an antigenic determinant recognized and bound by the T-cell receptor. Epitopes recognized by the T-cell receptor are often located in the inner, unexposed side of the antigen, and become accessible to the T-cell receptors after proteolytic processing of the antigen.

5 An "effective" immunization protocol is one in which an animal is protected against infection, at least to a measurable degree, when exposed to the specific infectious agent for which it was immunized.

An "ELISpot Assay" is a shorted name for "Enzyme-linked ImmunoSpot Assay", which refers to an antibody based method to detect secretion of soluble factors released by cells.
10 Originally developed as a method to detect antibody-secreting B-cells, later the method was adapted to determine T-cell reaction to a specific antigen, often represented as number of activated cells per million.

"Effective conditions" for culturing cells or cell lines means those culture conditions that allow the cells to respond in a manner than mimics or is the same as the response would be if the
15 cells were responding in vivo.

"Harvesting" cells or other materials means to separate and collect those cells from a mixture of from one source for use in another protocol.

A Bovine MHC class II bioassay, means an assay that measures the presence of a T cell-derived soluble factor, such as interferon (IFN- γ) release from T cells responding to specific
20 stimulation through the ability of IFN- γ to induce and up-regulate expression of class II molecules on bovine endothelial cells. Bovine endothelial cells do not constitutively express class II molecules unless triggered by external signals such as IFN- γ .

Since the list of technical and scientific terms cannot be all encompassing, any undefined terms shall be construed to have the same meaning as is commonly understood by one of skill in
25 the art to which this invention belongs. Furthermore, the singular forms "a", "an" and "the" include plural referents unless the context clearly dictates otherwise.

The invention is not to be limited only to the particular sequences, variants, formulations or methods described. The sequences, variants, formulations and methodologies may vary, and the terminology used herein is for the purpose of describing particular embodiments. The
30 terminology and definitions are not intended to be limiting.

Because of the redundancy of the genetic code, a variety of different DNA sequences can encode the amino acid sequences encoded by the polynucleotide sequences disclosed herein. It is

well within the skill of a person trained in the art to create these alternative DNA sequences encoding proteins having the same, or essentially the same, amino acid sequence. These variant DNA sequences are within the scope of the subject invention. As used herein, reference to "essentially the same" sequence refers to sequences that have amino acid substitutions, deletions, additions, or insertions that do not materially affect biological activity. Fragments retaining the characteristic biological activity are also included in this definition.

The subject invention comprises variant or equivalent proteins (and nucleotide sequences coding for equivalent proteins) having the same or similar biological activity of proteins encoded by the exemplified polynucleotides. Equivalent proteins will have amino acid similarity with an exemplified protein (or peptide). The amino acid identity will typically be greater than 60%. Preferably, the amino acid identity will be greater than 75%. More preferably, the amino acid identity will be greater than 80%, and even more preferably greater than 90%. Most preferably, amino acid identity will be greater than 95%. (Likewise, the polynucleotides that encode the subject polypeptides will also have corresponding identities in these preferred ranges.) These identities are as determined using standard alignment techniques for determining amino acid identity. The amino acid identity/similarity/homology will be highest in critical regions of the protein including those regions that account for biological activity or that are involved in the determination of three-dimensional configuration that is ultimately responsible for the biological activity. In this regard, certain amino acid substitutions are acceptable and can be expected if these substitutions are in regions which are not critical to activity or are conservative amino acid substitutions which do not affect the three-dimensional configuration of the molecule. For example, amino acids may be placed in the following classes: non-polar, uncharged polar, basic, and acidic. Conservative substitutions whereby an amino acid of one class is replaced with another amino acid of the same type fall within the scope of the subject invention so long as the substitution does not materially alter the biological activity of the compound. Below is a list of examples of amino acids belonging to various classes:

Nonpolar - Ala, Val, Leu, Ile, Pro, Met, Phe, Trp, uncharged polar Gly, Ser, Thr, Cys, Tyr, Asn, Gln

Acidic - Asp, Glu Basic Lys, His

In some instances, non-conservative substitutions can also be made.

As used herein, reference to "isolated" polynucleotides and/or "purified" proteins refers to these molecules when they are not associated with the other molecules with which they would

be found in nature. Thus, reference to "isolated" and/or "purified" signifies the involvement of the "hand of man" as described herein. Reference to "heterologous" proteins, genes, and gene constructs, also signifies the involvement of the "hand of man."

The invention also provides vectors containing the nucleic acid molecules described herein. The term "vector" refers to a vehicle, preferably a nucleic acid molecule, which can transport the nucleic acid molecules. When the vector is a nucleic acid molecule, the nucleic acid molecules are covalently linked to the vector nucleic acid. With this aspect of the invention, the vector includes a plasmid, single or double stranded phage, a single or double stranded RNA or DNA viral vector, or artificial chromosome, such as a BAC, PAC, YAC, OR MAC.

A vector can be maintained in the host cell as an extrachromosomal element where it replicates and produces additional copies of the nucleic acid molecules. Alternatively, the vector may integrate into the host cell genome and produce additional copies of the nucleic acid molecules when the host cell replicates.

The invention provides vectors for the maintenance (cloning vectors) or vectors for expression (expression vectors) of the nucleic acid molecules. The vectors can function in prokaryotic or eukaryotic cells or in both (shuttle vectors).

Expression vectors contain cis-acting regulatory regions that are operably linked in the vector to the nucleic acid molecules such that transcription of the nucleic acid molecules is allowed in a host cell. The nucleic acid molecules can be introduced into the host cell with a separate nucleic acid molecule capable of affecting transcription. Thus, the second nucleic acid molecule may provide a trans-acting factor interacting with the cis-regulatory control region to allow transcription of the nucleic acid molecules from the vector. Alternatively, a trans-acting factor may be supplied by the host cell. Finally, a trans-acting factor can be produced from the vector itself. It is understood, however, that in some embodiments, transcription and/or translation of the nucleic acid molecules can occur in a cell-free system.

The regulatory sequence to which the nucleic acid molecules described herein can be operably linked include promoters for directing mRNA transcription. These include, but are not limited to, the left promoter from bacteriophage .lambda., the lac, TRP, and TAC promoters from E. Coli, the early and late promoters from SV40, the CMV immediate early promoter, the adenovirus early and late promoters, and retrovirus long-terminal repeats.

In addition to control regions that promote transcription, expression vectors may also include regions that modulate transcription, such as repressor binding sites and enhancers.

Examples include the SV40 enhancer, the cytomegalovirus immediate early enhancer, polyoma enhancer, adenovirus enhancers, and retrovirus LTR enhancers.

In addition to containing sites for transcription initiation and control, expression vectors can also contain sequences necessary for transcription termination and, in the transcribed region a ribosome binding site for translation. Other regulatory control elements for expression include initiation and termination codons as well as polyadenylation signals. The person of ordinary skill in the art would be aware of the numerous regulatory sequences that are useful in expression vectors. Such regulatory sequences are described, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual*. 2nd. ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1989).

A variety of expression vectors can be used to express a nucleic acid molecule. Such vectors include chromosomal, episomal, and virus-derived vectors, for example vectors derived from bacterial plasmids, from bacteriophage, from yeast episomes, from yeast chromosomal elements, including yeast artificial chromosomes, from viruses such as baculoviruses, papovaviruses such as SV40, Vaccinia viruses including the modified vaccinia virus Ankara strain (MVA), adenoviruses, poxviruses including fowlpox virus (FP9), pseudorabies viruses, and retroviruses. Vectors may also be derived from combinations of these sources such as those derived from plasmid and bacteriophage genetic elements, e.g. cosmids and phagemids. Appropriate cloning and expression vectors for prokaryotic and eukaryotic hosts are described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*. 2nd. ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1989).

The regulatory sequence may provide constitutive expression in one or more host cells (i.e. tissue specific) or may provide for inducible expression in one or more cell types such as by temperature, nutrient additive, or exogenous factor such as a hormone or other ligand. A variety of vectors providing for constitutive and inducible expression in prokaryotic and eukaryotic hosts are well known to those of ordinary skill in the art.

The nucleic acid molecules can be inserted into the vector nucleic acid by well-known methodology. Generally, the DNA sequence that will ultimately be expressed is joined to an expression vector by cleaving the DNA sequence and the expression vector with one or more restriction enzymes and then ligating the fragments together. Procedures for restriction enzyme digestion and ligation are well known to those of ordinary skill in the art.

The vector containing the appropriate nucleic acid molecule can be introduced into an

appropriate host cell for propagation or expression using well-known techniques. Bacterial cells include, but are not limited to, *E. coli*, *Streptomyces*, and *Salmonella typhimurium*. Eukaryotic cells include, but are not limited to, yeast, insect cells such as *Drosophila*, animal cells such as COS and CHO cells, and plant cells.

5 As described herein, it may be desirable to express the peptide as a fusion protein. Accordingly, the invention provides fusion vectors that allow for the production of the peptides. Fusion vectors can increase the expression of a recombinant protein, increase the solubility of the recombinant protein, and aid in the purification of the protein by acting for example as a ligand for affinity purification. A proteolytic cleavage site may be introduced at the junction of the
10 fusion moiety so that the desired peptide can ultimately be separated from the fusion moiety. Proteolytic enzymes include, but are not limited to, factor Xa, thrombin, and enteroenzyme. Typical fusion expression vectors include pGEX (Smith et al., Gene 67:31-40 (1988)), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the
15 target recombinant protein. Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann et al, Gene 69:301-315 (1988)) and pET 11d (Studier et al, Gene Expression Technology: Methods in Enzymology 185:60-89 (1990)).

 Recombinant protein expression can be maximized in host bacteria by providing a genetic background wherein the host cell has an impaired capacity to proteolytically cleave the
20 recombinant protein. (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990) 119-128). Alternatively, the sequence of the nucleic acid molecule of interest can be altered to provide preferential codon usage for a specific host cell, for example *E. coli*. (Wada et al., Nucleic Acids Res. 20:2111-2118 (1992)).

 The nucleic acid molecules can also be expressed by expression vectors that are
25 operative in yeast. Examples of vectors for expression in yeast e.g., *S. cerevisiae* include pYepSecI (Baldari, et al, EMBO J. 6:229-234 (1987)), pMFa (Kujan et al, Cell 30:933-943(1982)), pJRY88 (Schultz et al, Gene 54:113-123 (1987)), and pYES2 (Invitrogen Corporation, San Diego, Calif.).

 The nucleic acid molecules can also be expressed in insect cells using, for example,
30 baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf9 cells) include the pAc series (Smith et al, Mol. Cell Biol. 3:2156-2165 (1983)) and the pVL series (Lucklow et al, Virology 170:31-39 (1989)).

In certain embodiments of the invention, the nucleic acid molecules described herein are expressed in mammalian cells using mammalian expression vectors. Examples of mammalian expression vectors include pCDM8 (Seed, B. Nature 329:840(1987)) and pMT2PC (Kaufman et al., EMBO J. 6:187-195 (1987)).

5 The expression vectors listed herein are provided by way of example only of the well-known vectors available to those of ordinary skill in the art that would be useful to express the nucleic acid molecules. The person of ordinary skill in the art would be aware of other vectors suitable for maintenance propagation or expression of the nucleic acid molecules described herein. These are found for example in Sambrook, J., Fritsh, E. F., and Maniatis, T. Molecular
10 Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

The invention also encompasses vectors in which the nucleic acid sequences described herein are cloned into the vector in reverse orientation, but operably linked to a regulatory sequence that permits transcription of antisense RNA. Thus, an antisense transcript can be
15 produced to all, or to a portion, of the nucleic acid molecule sequences described herein, including both coding and non-coding regions. Expression of this antisense RNA is subject to each of the parameters described above in relation to expression of the sense RNA (regulatory sequences, constitutive or inducible expression, tissue-specific expression).

The invention also relates to recombinant host cells containing the vectors described
20 herein. Host cells therefore include prokaryotic cells, lower eukaryotic cells such as yeast, other eukaryotic cells such as insect cells, and higher eukaryotic cells such as mammalian cells.

The recombinant host cells are prepared by introducing the vector constructs described herein into the cells by techniques readily available to the person of ordinary skill in the art. These include, but are not limited to, calcium phosphate transfection, DEAE-dextran-mediated
25 transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, lipofection, and other techniques such as those found in Sambrook, et al. (Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989).

Host cells can contain more than one vector. Thus, different nucleotide sequences can be
30 introduced on different vectors of the same cell. Similarly, the nucleic acid molecules can be introduced either alone or with other nucleic acid molecules that are not related to the nucleic acid molecules such as those providing trans-acting factors for expression vectors. When more than

one vector is introduced into a cell, the vectors can be introduced independently, co-introduced or joined to the nucleic acid molecule vector.

In the case of bacteriophage and viral vectors, these can be introduced into cells as packaged or encapsulated virus by standard procedures for infection and transduction. Viral
5 vectors can be replication-competent or replication-defective. In the case in which viral replication is defective, replication will occur in host cells providing functions that complement the defects.

Vectors generally include selectable markers that enable the selection of the subpopulation of cells that contain the recombinant vector constructs. The marker can be
10 contained in the same vector that contains the nucleic acid molecules described herein or may be on a separate vector. Markers include tetracycline or ampicillin-resistance genes for prokaryotic host cells and dihydrofolate reductase or neomycin resistance for eukaryotic host cells. However, any marker that provides selection for a phenotypic trait will be effective.

While the mature proteins can be produced in bacteria, yeast, mammalian cells, and other
15 cells under the control of the appropriate regulatory sequences, cell-free transcription and translation systems can also be used to produce these proteins using RNA derived from the DNA constructs described herein.

Where secretion of the peptide is desired, which is difficult to achieve with multi-transmembrane domain containing proteins such as MHC Class I-binding peptides, appropriate
20 secretion signals are incorporated into the vector. The signal sequence can be endogenous to the peptides or heterologous to these peptides.

The expressed protein can be isolated from the host cell by standard disruption procedures, including freeze thaw, sonication, mechanical disruption, use of lysing agents and the like. The peptide can then be recovered and purified by well-known purification methods
25 including ammonium sulfate precipitation, acid extraction, anion or cationic exchange chromatography, phosphocellulose chromatography, hydrophobic-interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography, or high performance liquid chromatography.

It is also understood that depending upon the host cell in recombinant production of the
30 peptides described herein, the peptides can have various glycosylation patterns, depending upon the cell, or maybe non-glycosylated as when produced in bacteria. In addition, the peptides may include an initial modified methionine in some cases as a result of a host-mediated process.

There are many methods for introducing a heterologous gene or polynucleotide into a host cell or cells under conditions that allow for stable maintenance and expression of the gene or polynucleotide. These methods are well known to those skilled in the art. Synthetic genes, such as, for example, those genes modified to enhance expression in a heterologous host (such as by preferred codon usage or by the use of adjoining, downstream, or upstream enhancers) that are functionally equivalent to the genes (and which encode equivalent proteins) can also be used to transfect hosts. Methods for the production of synthetic genes are known in the art. Recombinant hosts can be used for the expression or propagation of genes and polynucleotides of the present invention. The genes and polynucleotides within the scope of the present invention can be introduced into a wide variety of microbial or plant hosts, such as bacterial cells, yeast, insect cells, plant cell cultures or plants, mammalian cells. For example, *T. parva* nucleic acids can be expressed in a recombinant baculovirus (BV) possessing an optimized promoter and translation initiation region operably linked to the *T. parva* nucleic acid. In a preferred embodiment, an optimized promoter and translation initiation region are operably linked to the *T. parva* nucleic acid. In one embodiment, insect host cells can be transformed with baculovirus expressing *T. parva* nucleic acids. In still another embodiment, Tn5 (*Trichoplusia ni* or High Five.TM.) host cells can be transformed with baculovirus expressing *T. parva* nucleic acids.

T. parva "recombinant protein", is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions,

insertions and/or deletions, as discussed below.

Included in the definition of *T. parva* antigen polypeptides are *T. parva* polypeptide variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding a *T. parva* antigen polypeptide, using cassette or PCR mutagenesis, scanning mutagenesis, gene shuffling or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant *T. parva* polypeptide fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the *T. parva* antigen polypeptide amino acid sequence.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed *T. parva* antigen polypeptide variants can be screened for the optimal combination of desired activity. Techniques for making mutations at predetermined sites in DNA having a known sequence are well known. For example, the variations can be made using oligonucleotide-mediated site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)], all of which are expressly incorporated by reference, PCR mutagenesis, or other known techniques can be performed on the cloned DNA to produce *T. parva* antigen polypeptide variant DNA. Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989), which is expressly incorporated by reference]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976),

which are expressly incorporated by reference]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used. Screening of the mutants or variants is done using Elispot and/or bioassays of T. parva antigen polypeptide activities and/or properties as described herein.

5 The present invention further provides fragments of the antigen peptides, in addition to proteins and peptides that comprise and consist of such fragments, particularly those comprising the residues identified in SEQ ID NO:9-17. The fragments to which the invention pertains, however, are not to be construed as encompassing fragments that may be disclosed publicly prior to the present invention.

10 As used herein, a fragment comprises at least about 8, 10, 12, 14, 16, or more contiguous amino acid residues from an antigen peptide. Such fragments can be chosen based on the ability to retain one or more of the biological activities of the antigen peptide or could be chosen for the ability to perform a function, e.g. bind a substrate or act as an immunogen. Particularly important fragments are biologically active fragments, peptides that are, for example, about 8 or more amino
15 acids in length. Such fragments will typically comprise a domain or motif of the antigen peptide, e.g., active site, a transmembrane domain or a substrate-binding domain. Further, possible fragments include, but are not limited to, domain or motif containing fragments, soluble peptide fragments, and fragments containing immunogenic structures. Predicted domains and functional sites are readily identifiable by computer programs well known and readily available to those of
20 skill in the art (e.g., PROSITE analysis).

 Polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally occurring amino acids. Further, many amino acids, including the terminal amino acids, may be modified by natural processes, such as processing and other post-translational modifications, or by chemical modification techniques well known in the art.
25 Common modifications that occur naturally in antigen peptides are described in basic texts, detailed monographs, and the research literature, and they are well known to those of skill in the art.

 Known modifications include, but are not limited to, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety,
30 covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of

pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

5 Such modifications are well known to those of skill in the art and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as *Proteins--Structure and Molecular Properties*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York
10 (1993). Many detailed reviews are available on this subject, such as by Wold, F., *Posttranslational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York 1-12 (1983); Seifter et al. (*Meth. Enzymol.* 182: 626-646 (1990)) and Rattan et al. (*Ann. N.Y Acad. Sci.* 663:48-62 (1992)).

 Accordingly, the antigen peptides of the present invention also encompass derivatives or
15 analogs in which a substituted amino acid residue is not one encoded by the genetic code, in which a substituent group is included, in which the mature antigen peptide is fused with another compound, such as a compound to increase the half-life of the antigen peptide (for example, polyethylene glycol), or in which the additional amino acids are fused to the mature antigen peptide, such as a leader or secretory sequence or a sequence for purification of the mature antigen
20 peptide or a pro-protein sequence.

 Although an amino acid sequence or oligopeptide used for antibody induction does not require biological activity, it must be immunogenic. A peptide, polypeptide, or protein used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids and preferably at least 10 amino acids. Short stretches of amino acid sequence may be genetically
25 or chemically fused with those of another protein such as keyhole limpet hemocyanin, and the chimeric peptide used for antibody production. Alternatively, the oligopeptide may be of sufficient length to contain an entire domain.

 Antibodies specific for peptides, polypeptides, or proteins may be produced by inoculation of an appropriate animal with an antigenic fragment of the peptide, polypeptide, or
30 protein. Antibody production includes not only the stimulation of an immune response by injection into animals, but also analogous processes such as the production of synthetic antibodies, the screening of recombinant immunoglobulin libraries for specific-binding molecules (Orlandi R.

et al. [1989] PNAS 86:3833-3837, or Huse W. D. et al. [1989] Science 256:1275-1281), or the in vitro stimulation of lymphocyte populations. Current technology (Winter G. and Milstein C. [1991] Nature 349:293-299) provides for a number of highly specific binding reagents based on the principles of antibody formation. These techniques may be adapted to produce molecules which specifically bind antigen peptides. Antibodies or other appropriate molecules generated against a specific immunogenic peptide fragment or oligopeptide can be used in Western analysis, enzyme-linked immunosorbent assays (ELISA) or similar tests to establish the presence of or to quantitate amounts of peptide, polypeptide, or protein in normal, diseased, or transformed cells, tissues, organs, or organisms as well as liquid suspensions containing said peptide, polypeptide, or protein.

The invention also provides antibodies that selectively bind to one of the peptides of the present invention, a protein comprising such a peptide, as well as variants and fragments thereof. As used herein, an antibody selectively binds a target peptide when it binds the target peptide and does not significantly bind to unrelated proteins. An antibody is still considered to selectively bind a peptide even if it also binds to other proteins that are not substantially homologous with the target peptide so long as such proteins share homology with a fragment or domain of the peptide target of the antibody. In this case, it would be understood that antibody binding to the peptide is still selective despite some degree of cross-reactivity.

As used herein, an antibody is defined in terms consistent with that recognized within the art: they are multi-subunit proteins produced by a mammalian organism in response to an antigen challenge. The antibodies of the present invention include polyclonal antibodies and monoclonal antibodies, as well as fragments of such antibodies, including, but not limited to, Fab or F(ab')₂, and Fv fragments.

Many methods are known for generating and/or identifying antibodies to a given target peptide. Several such methods are described by Harlow, Antibodies, Cold Spring Harbor Press, (1989).

In general, to generate antibodies, an isolated peptide is used as an immunogen and is administered to a mammalian organism, such as a rat, rabbit or mouse. The full-length protein, an antigenic peptide fragment or a fusion protein can be used. Particularly important fragments are those covering functional domains, such as the domains identified in the figures, and domain of sequence homology or divergence amongst the family, such as those that can readily be identified using protein alignment methods and as presented in the Figures.

Antibodies are preferably prepared from regions or discrete fragments of the antigen proteins. Antibodies can be prepared from any region of the peptide as described herein. However, preferred regions will include those involved in function/activity and/or antigen/binding partner interaction.

5 An antigenic fragment will typically comprise at least 8 contiguous amino acid residues. The antigenic peptide can comprise, however, at least 10, 12, 14, 16 or more amino acid residues. Such fragments can be selected on a physical property, such as fragments correspond to regions that are located on the surface of the protein, e.g., hydrophilic regions or can be selected based on sequence uniqueness.

10 Detection on an antibody of the present invention can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta.-galactosidase, or acetylcholinesterase;
15 examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include
20 ^{125}I , ^{131}I , ^{35}S or ^3H .

 The antibodies can be used to isolate one of the proteins of the present invention by standard techniques, such as affinity chromatography or immunoprecipitation. The antibodies can facilitate the purification of the natural protein from cells and recombinantly produced protein expressed in host cells. In addition, such antibodies are useful to detect the presence of one of the
25 proteins of the present invention in cells or tissues to determine the pattern of expression of the protein among various tissues in an organism and over the course of schizont development. Such antibodies can be used to detect protein in situ, in vitro, or in a cell lysate or supernatant in order to evaluate the abundance and pattern of expression. Also, such antibodies can be used to assess abnormal tissue distribution or abnormal expression during development or progression of a
30 protozoan infection. Antibody detection of circulating fragments of the full length protein can be used to identify turnover.

 Further, the antibodies can be used to assess expression in disease states such as in active

stages of the disease or in lymphocytes harvested from infected animals. Experimental data as provided in FIG. 16 indicates expression in bovine lymphocytes, infected with *T. parva*. If a disease is characterized by a specific mutation in the protein, antibodies specific for this mutant protein can be used to assay for the presence of the specific mutant protein.

5 The diagnostic uses can be applied, not only in genetic testing, but also in monitoring a treatment modality. Accordingly, where treatment is ultimately aimed at preventing or controlling infection, antibodies directed against the protein or relevant fragments can be used to monitor therapeutic efficacy.

10 The antibodies are also useful for inhibiting protein function, for example, blocking the binding of the antigenic peptide to a binding partner such as a substrate. These uses can also be applied in a therapeutic context in which treatment involves inhibiting the protein's function. An antibody can be used, for example, to block binding, thus modulating (agonizing or antagonizing) the peptides activity. Antibodies can be prepared against specific fragments containing sites required for function or against intact protein that is associated with a cell or cell membrane. See
15 SEQ ID NO: 1-7 and 9-17 and Fig. 9 and 10, for structural information relating to the proteins of the present invention.

20 The invention also encompasses kits for using antibodies to detect the presence of a protein in a biological sample. The kit can comprise antibodies such as a labeled or labelable antibody and a compound or agent for detecting protein in a biological sample; means for determining the amount of protein in the sample; means for comparing the amount of protein in the sample with a standard; and instructions for use. Such a kit can be supplied to detect a single protein or epitope or can be configured to detect one of a multitude of epitopes, such as in an antibody detection array. Arrays are described in detail below for nucleic acid arrays and similar
25 methods have been developed for antibody arrays.

30 The proteins of the present invention can be used in assays related to the functional information provided in the Figures; for example, to stimulate CD8+ cytotoxic T cell lines, to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; and as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state). Where the protein binds or potentially binds to another protein or ligand (such as, for example, in a enzyme-effector protein interaction or enzyme-ligand

interaction), the protein can be used to identify the binding partner/ligand so as to develop a system to identify inhibitors of the binding interaction. Any or all of these uses are capable of being developed into reagent grade or kit format for commercialization as commercial products.

Methods for performing the uses listed above are well known to those skilled in the art.

- 5 References disclosing such methods include "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

- 10 The potential uses of the peptides of the present invention are based primarily on the source of the protein as well as the class/action of the protein. For example, antigens isolated from *T. parva* and their protozoan orthologs serve as targets for identifying agents for use in mammalian therapeutic applications, e.g. an animal drug, particularly in modulating a biological or pathological response in a cell, tissue, or protozoan, that expresses an immunogenic antigen. Experimental data as provided in FIG. 16 indicates that the antigens of the present invention are
15 expressed in infected host lymphocytes, as indicated by flow cytometric analysis. Such uses can readily be determined using the information provided herein, that which is known in the art, and routine experimentation.

- To perform assays of the invention, such as assays to detect a pathogen, e.g., by detecting the presence and/or expression of a polypeptide of the invention in the pathogen, it is
20 sometimes desirable to immobilize either the antigen protein, or fragment, or its target molecule to facilitate separation of complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay.

- Techniques for immobilizing proteins on matrices can be used in assays of the invention. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein
25 to be bound to a matrix. For example, glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, Mo.) or glutathione derivatized microtitre plates, which are then combined with the cell lysates (e.g., ³⁵S-labeled) and the candidate compound, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads are washed to
30 remove any unbound label, and the matrix immobilized and radiolabel determined directly, or in the supernatant after the complexes are dissociated. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of antigen-binding protein

found in the bead fraction quantitated from the gel using standard electrophoretic techniques. For example, either the polypeptide or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin using techniques well known in the art. Alternatively, antibodies reactive with the protein but which do not interfere with binding of the protein to its target molecule can be derivatized to the wells of the plate, and the protein trapped in the wells by antibody conjugation. Preparations of an antigen-binding protein and a candidate compound are incubated in the antigen protein-presenting wells and the amount of complex trapped in the well can be quantitated. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the antigen protein target molecule, or which are reactive with antigen protein and compete with the target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the presence of the target molecule.

The antigen proteins of the present invention are also useful to provide a target for diagnosing a disease or a disease mediated by the peptide. Accordingly, the invention provides methods for detecting the presence, or levels of, the protein (or encoding mRNA) in a cell, tissue, or organism. Experimental data as provided in FIG. 16 indicates expression in *T. parva*-infected bovine lymphocytes. The method involves contacting a biological sample with a compound capable of interacting with the antigen protein such that the interaction can be detected. Such an assay can be provided in a single detection format or a multi-detection format such as an antibody chip array.

One agent for detecting a protein in a sample is an antibody capable of selectively binding to protein. A biological sample includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject.

The peptides of the present invention also provide targets for diagnosing active parasite activity or disease, in an animal having a variant peptide, particularly activities and conditions that are known for other members of the family of proteins to which the present one belongs. Thus, the peptide can be isolated from a biological sample and assayed for the presence of a genetic mutation that results in aberrant peptide. This includes amino acid substitution, deletion, insertion, rearrangement, (as the result of aberrant splicing events), and inappropriate post-translational modification. Analytic methods include altered electrophoretic mobility, altered tryptic peptide digest, altered enzyme activity in cell-based or cell-free assay, alteration in substrate or antibody-binding pattern, altered isoelectric point, direct amino acid sequencing, and any other of the

known assay techniques useful for detecting mutations in a protein. Such an assay can be provided in a single detection format or a multi-detection format such as an antibody chip array.

In vitro techniques for detection of peptide include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence using a detection
5 reagent, such as an antibody or protein binding agent, as well as the methods that represent embodiments of the present invention. Alternatively, the peptide can be detected in vivo in a subject by introducing into the subject a labeled anti-peptide antibody or other types of detection agent. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques. Such methods can be used to
10 detect the allelic variant of a peptide expressed in an infected subject and methods which detect fragments of a peptide in a sample.

The diagnostic uses can be applied, not only in genetic testing, but also in monitoring a treatment modality. Accordingly, where treatment is ultimately aimed at preventing or controlling infection, antibodies directed against the protein or relevant fragments can be used to monitor
15 therapeutic efficacy.

The invention also encompasses kits for using antibodies to detect the presence of a protein in a biological sample. The kit can comprise antibodies such as a labeled or labelable antibody and a compound or agent for detecting protein in a biological sample; means for determining the amount of protein in the sample; means for comparing the amount of protein in
20 the sample with a standard; and instructions for use. Such a kit can be supplied to detect a single protein or epitope or can be configured to detect one of a multitude of epitopes, such as in an antibody detection array. Arrays are described in detail below for nucleic acid arrays and similar methods have been developed for antibody arrays.

The present invention further provides isolated nucleic acid molecules that encode a T.
25 parva antigen peptide or protein of the present invention (cDNA, transcript and genomic sequence). Such nucleic acid molecules will consist of, consist essentially of, or comprise a nucleotide sequence that encodes one of the enzyme peptides of the present invention, an allelic variant thereof, or an ortholog or paralog thereof.

As used herein, an "isolated" nucleic acid molecule is one that is separated from other
30 nucleic acid present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is

derived. However, there can be some flanking nucleotide sequences, for example up to about 5KB, 4KB, 3KB, 2KB, or 1KB or less, particularly contiguous peptide encoding sequences and peptide encoding sequences within the same gene but separated by introns in the genomic sequence. The important point is that the nucleic acid is isolated from remote and unimportant flanking sequences such that it can be subjected to the specific manipulations described herein such as recombinant expression, preparation of probes and primers, and other uses specific to the nucleic acid sequences.

Moreover, an "isolated" nucleic acid molecule, such as a transcript/cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. However, the nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated.

For example, recombinant DNA molecules contained in a vector are considered isolated. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include in vivo or in vitro RNA transcripts of the isolated DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

The nucleic acid may be double stranded, single stranded, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences depicted in the figures also include the complement of the sequence.

As disclosed herein, 100% sequence identity between the RNA and the target gene is not required to practice the present invention. Thus the invention has the advantage of being able to tolerate sequence variations that might be expected due to genetic mutation, strain polymorphism, or evolutionary divergence. RNAi molecules of the subject invention are not limited to those that are targeted to the full-length polynucleotide or gene. Gene product can be inhibited with a RNAi molecule that is targeted to a portion or fragment of the exemplified polynucleotides; high homology (90-95%) or greater identity is also preferred, but not necessarily essential, for such applications.

Accordingly, the present invention provides nucleic acid molecules that consist of, consist essentially of, or comprise, the nucleotide sequence shown in SEQ ID NO: 18-22 or any

nucleic acid molecule that encodes a protein encoded by SEQ ID NO: 18-22 (as shown, *e.g.*, in Figures 9, 10, and 17).

The term "consisting essentially of," when used in the context of biopolymers, refers to a sequence which is intermediate between the number of residues (amino acids or, in the present case, nucleotides) encompassed by the term "consisting of" and the longer length encompassed by the term "comprising." Residues in addition to the residues encompassed by "consisting of" language do not affect the basic and novel characteristics (*e.g.*, in the case of a polynucleotide, the ability to encode a functional peptide, or to bind specifically to a nucleic acid of interest) of the molecule encompassed by the "consisting of" language.

The invention further provides nucleic acid molecules that encode fragments of the peptides of the present invention as well as nucleic acid molecules that encode obvious variants of the enzyme proteins of the present invention that are described above. Such nucleic acid molecules may be naturally occurring, such as allelic variants (same locus), paralogs (different locus), and orthologs (different organism), or may be constructed by recombinant DNA methods or by chemical synthesis. Such non-naturally occurring variants may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells, or organisms. Accordingly, as discussed above, the variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions.

The present invention further provides epitope fragments of the antigen proteins and the nucleic acid molecules encoding the antigens, provided in the description of epitope-mapping experiments described below. An epitope coding region comprises a contiguous nucleotide sequence greater than 12 or more nucleotides. Further, a fragment could at least 30, 40, 50, 100, 250 or 500 nucleotides in length. The length of the fragment will be based on its intended use. For example, the fragment can encode epitope bearing regions of the peptide, or can be useful as DNA probes and primers. Such fragments can be isolated using the known nucleotide sequence to synthesize an oligonucleotide probe. A labeled probe can then be used to screen a cDNA library, genomic DNA library, or mRNA to isolate nucleic acid corresponding to the coding region. Further, primers can be used in PCR reactions to clone specific regions of gene.

A probe/primer typically comprises substantially a purified oligonucleotide or oligonucleotide pair. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 20, 25, 40, 50 or more consecutive

nucleotides.

Orthologs, homologs, and allelic variants can be identified using methods well known in the art. As described in the Peptide Section, these variants comprise a nucleotide sequence encoding a peptide that is typically 60-70%, 70-80%, 80-90%, and more typically at least about
5 90-95% or more homologous to the nucleotide sequence shown in the Figure sheets or a fragment of this sequence. Such nucleic acid molecules can readily be identified as being able to hybridize under moderate to stringent conditions, to the nucleotide sequence shown in the Figure sheets or a fragment of the sequence. Allelic variants can readily be determined by genetic locus of the encoding gene. The gene encoding the novel enzyme of the present invention is located on a
10 genome component that has been mapped to the *T. parva* chromosome 1 and 2 which is supported by multiple lines of evidence, such as STS and BAC map data.

The nucleic acid molecules of the present invention are useful as probes, primers, chemical intermediates, and in biological assays. The nucleic acid molecules are useful as a hybridization probe for messenger RNA, transcript/cDNA and genomic DNA to isolate full-length
15 cDNA and genomic clones encoding the peptide described in SEQ ID NO:9-17 and to isolate cDNA and genomic clones that correspond to variants (alleles, orthologs, etc.) producing the same or related peptides shown in SEQ ID NO:1-7 and 9-17. As illustrated in FIG. 10, deletions were identified at 2 different nucleotide positions.

The probe can correspond to any sequence along the entire length of the nucleic acid
20 molecules provided in the SEQ ID information. Accordingly, it could be derived from 5' noncoding regions, the coding region, and 3' noncoding regions. However, as discussed, fragments are not to be construed as encompassing fragments disclosed prior to the present invention.

The nucleic acid molecules are also useful as primers for PCR to amplify any given region of a nucleic acid molecule and are useful to synthesize antisense molecules of desired
25 length and sequence.

The nucleic acid molecules are also useful for constructing recombinant vectors. Such vectors include expression vectors that express a portion of, or all of, the peptide sequences. Vectors also include insertion vectors, used to integrate into another nucleic acid molecule sequence, such as into the cellular genome, to alter in situ expression of a gene and/or gene
30 product. For example, an endogenous coding sequence can be replaced via homologous recombination with all or part of the coding region containing one or more specifically introduced mutations.

The nucleic acid molecules are also useful for expressing antigenic portions of the proteins.

The nucleic acid molecules are also useful as probes for determining the chromosomal positions of the nucleic acid molecules by means of in situ hybridization methods. The genes
5 encoding the novel antigens of the present invention are located on a genome component that has been mapped to *T. parva* chromosomes 1 (Tp1 & Tp4) and 2 (Tp5, Tp7 & Tp8).

The nucleic acid molecules are also useful in making vectors containing the gene regulatory regions of the nucleic acid molecules of the present invention.

The nucleic acid molecules are also useful for designing antigens corresponding to all, or
10 a part, of the mRNA produced from the nucleic acid molecules described herein.

The nucleic acid molecules are also useful for making vectors that express part, or all, of the peptides.

The nucleic acid molecules are also useful for constructing host cells expressing a part, or all, of the nucleic acid molecules and peptides.

15 The nucleic acid molecules are also useful as hybridization probes for determining the presence, level, form and distribution of nucleic acid expression. Such probes could be used to detect the presence of, or to determine levels of, a specific nucleic acid molecule in cells, tissues, and in organisms. The nucleic acid whose level is determined can be DNA or RNA. Accordingly, probes corresponding to the peptides described herein can be used to assess expression and/or
20 gene copy number in a given cell, tissue, or organism. These uses are relevant for diagnosis of disorders involving an increase or decrease in antigen protein expression relative to normal results.

In vitro techniques for detection of mRNA include Northern hybridizations and in situ hybridizations. In vitro techniques for detecting DNA includes Southern hybridizations and in situ hybridization.

25 Probes can be used as a part of a diagnostic test kit for identifying cells or tissues that express an *T. parva* antigen protein, such as by measuring a level of an antigen-encoding nucleic acid in a sample of cells from a subject e.g., mRNA or genomic DNA, or determining if an antigen gene has been mutated.

30 The invention encompasses kits for detecting the presence of an antigen nucleic acid in a biological sample. For example, the kit can comprise reagents such as a labeled or labelable nucleic acid or agent capable of detecting antigen nucleic acid in a biological sample; means for determining the amount of antigen nucleic acid in the sample; and means for comparing the

amount of antigen nucleic acid in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect antigen protein mRNA or DNA.

5 The present invention further provides nucleic acid detection kits, such as arrays or microarrays of nucleic acid molecules that are based on the sequence information provided in SEQ ID NO: 18-31.

As used herein "Arrays" or "Microarrays" refers to an array of distinct polynucleotides or oligonucleotides synthesized on a substrate, such as paper, nylon or other type of membrane, filter, chip, glass slide, or any other suitable solid support. In one embodiment, the microarray is
10 prepared and used according to the methods described in U.S. Pat. No. 5,837,832, Chee et al., PCT application W095/11995 (Chee et al.), Lockhart, D. J. et al. (1996; Nat. Biotech. 14: 1675-1680) and Schena, M. et al. (1996; Proc. Natl. Acad. Sci. 93: 10614-10619), all of which are incorporated herein in their entirety by reference. In other embodiments, such arrays are produced by the methods described by Brown et al., U.S. Pat. No. 5,807,522.

15 The microarray or detection kit is preferably composed of a large number of unique, single-stranded nucleic acid sequences, usually either synthetic antisense oligonucleotides or fragments of cDNAs, fixed to a solid support. The oligonucleotides are preferably about 6-60 nucleotides in length, more preferably 15-30 nucleotides in length, and most preferably about 20-25 nucleotides in length. For a certain type of microarray or detection kit, it may be preferable to
20 use oligonucleotides that are only 7-20 nucleotides in length. The microarray or detection kit may contain oligonucleotides that cover the known 5', or 3', sequence, sequential oligonucleotides which cover the full length sequence; or unique oligonucleotides selected from particular areas along the length of the sequence. Polynucleotides used in the microarray or detection kit may be oligonucleotides that are specific to a gene or genes of interest.

25 In order to produce oligonucleotides to a known sequence for a microarray or detection kit, the gene(s) of interest (or an ORF identified in the present invention) is typically examined using a computer algorithm which starts at the 5' or at the 3' end of the nucleotide sequence. Typical algorithms will then identify oligomers of defined length that are unique to the gene, have a GC content within a range suitable for hybridization, and lack predicted secondary structure that
30 may interfere with hybridization. In certain situations it may be appropriate to use pairs of oligonucleotides on a microarray or detection kit. The "pairs" will be identical, except for one nucleotide that preferably is located in the center of the sequence. The second oligonucleotide in

the pair (mismatched by one) serves as a control. The number of oligonucleotide pairs may range from two to one million. The oligomers are synthesized at designated areas on a substrate using a light-directed chemical process. The substrate may be paper, nylon or other type of membrane, filter, chip, glass slide or any other suitable solid support.

5 In another aspect, an oligonucleotide may be synthesized on the surface of the substrate by using a chemical coupling procedure and an ink jet application apparatus, as described in PCT application W095/251116 (Baldeschweiler et al.) which is incorporated herein in its entirety by reference. In another aspect, a "gridded" array analogous to a dot (or slot) blot may be used to
10 arrange and link cDNA fragments or oligonucleotides to the surface of a substrate using a vacuum system, thermal, UV, mechanical or chemical bonding procedures. An array, such as those described above, may be produced by hand or by using available devices (slot blot or dot blot apparatus), materials (any suitable solid support), and machines (including robotic instruments), and may contain 8, 24, 96, 384, 1536, 6144 or more oligonucleotides, or any other number
15 between two and one million which lends itself to the efficient use of commercially available instrumentation.

In order to conduct sample analysis using a microarray or detection kit, the RNA or DNA from a biological sample is made into hybridization probes. The mRNA is isolated, and cDNA is produced and used as a template to make antisense RNA (aRNA). The aRNA is amplified in the presence of fluorescent nucleotides, and labeled probes are incubated with the
20 microarray or detection kit so that the probe sequences hybridize to complementary oligonucleotides of the microarray or detection kit. Incubation conditions are adjusted so that hybridization occurs with precise complementary matches or with various degrees of less complementarity. After removal of nonhybridized probes, a scanner is used to determine the levels and patterns of fluorescence. The scanned images are examined to determine degree of
25 complementarity and the relative abundance of each oligonucleotide sequence on the microarray or detection kit. The biological samples may be obtained from any bodily fluids (such as blood, urine, saliva, phlegm, gastric juices, etc.), cultured cells, biopsies, or other tissue preparations. A detection system may be used to measure the absence, presence, and amount of hybridization for all of the distinct sequences simultaneously. This data may be used for large-scale correlation
30 studies on the sequences, expression patterns, mutations, variants, or polymorphisms among samples.

Using such arrays, the present invention provides methods to identify the presence or

expression of the antigen proteins/peptides of the present invention. In detail, such methods comprise incubating a test sample with one or more nucleic acid molecules and assaying for binding of the nucleic acid molecule with components within the test sample. Such assays will typically involve arrays comprising many genes, at least one of which is a gene of the present invention and or alleles of the enzyme gene of the present invention. The figures and associated information below provide information on epitope sequence and micro-variation in strains of *T. parva*, that have been found in the gene encoding the antigen of the present invention.

Conditions for incubating a nucleic acid molecule with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid molecule used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or array assay formats can readily be adapted to employ the novel fragments of the *T. parva* genome disclosed herein. Examples of such assays can be found in Chard, T, An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G. R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, Fla. Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

The test samples of the present invention include cells, protein or membrane extracts of cells. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing nucleic acid extracts or of cells are well known in the art and can be readily be adapted in order to obtain a sample that is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the nucleic acid molecules that can bind to a fragment of the *T. parva* genome disclosed herein; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound nucleic acid.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers, strips of

plastic, glass or paper, or arraying material such as silica. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container
5 which will accept the test sample, a container which contains the nucleic acid probe, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound probe. One skilled in the art will readily recognize that the previously unidentified enzyme gene of the present invention can be routinely identified using the sequence information disclosed herein can be readily incorporated into one of
10 the established kit formats which are well known in the art, particularly expression arrays.

The *T. parva* antigens of the present invention have particular potential for induction of in vivo, antigen-specific CD8+ cytotoxic T cells for prophylactic immunization of cattle for the prevention of East Coast Fever disease. In addition, CTLs specific to the following metazoan parasites may also be induced by compositions identified in accordance with the methods of the
15 present invention: *Plasmodium falciparum* (which causes malaria), *Schistosoma mansoni* (which causes schistosomiasis), and *Trypanosoma cruzi* (which causes Chagas' disease), *Giardia lamblia*, *Entamoeba histolytica*, *Cryptosporidium* spp., *Leishmania* spp., *Brugia* spp., *Wuchereria* spp., *Onchocerca* spp., *Strongyloides* spp., *Coccidia*, *Haemaphysalis* spp., *Ostertagia* spp., *Trichomonas* spp., *Dirofilaria* spp., *Toxocara* spp., *Naegleria* spp., *Pneumocystis carinii*, *Ascaris* spp., other
20 *Trypanosoma* spp., other *Schistosoma* spp., other *Plasmodium* spp., *Babesia* spp., *Theileria* spp., including but not limited to *T. parva*, *T. lawrencei*, *T. annulata*, *T. hirci*, *T. ovis*, *T. lastoguardi*, *T. orientalis*, *T. buffeli* and *T. taurotragi*, *Babesia* spp., including, but not limited to *B. bigemina*, *B. divergens*, *B. major*, *B. bovis*, *B. motasi*, *B. ovis*, *B. cabelli*, *B. equi*, *B. traumani*, *B. canis*, *B. gibsoni*, *B. felis*, and *B. microfti*, *Adelina* spp., including, but not limited to *A. delina*, *A. castana*,
25 *A. picei*, *A. palori*, and *A. triboli*, *Anisakis* and *Isospora* *beli*.

Following are examples which illustrate procedures for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted. As used herein and further defined
30 below, "nucleic acid" may refer to either DNA or RNA, or molecules which contain both deoxy- and ribonucleotides. The nucleic acids include genomic DNA, cDNA, and oligonucleotides including sense and anti-sense nucleic acids. Such nucleic acids may also contain modifications in

the ribose-phosphate backbone to increase stability and half life of such molecules in physiological environments.

EXAMPLES

Generation of a unidirectional cDNA expression library of *Theileria parva* schizont stage

5 Generation of *Theileria parva* Muguga-infected cell lines (TpM) --Peripheral blood mononuclear cells (PBMC) were isolated from venous blood and infected with *T. parva* (Muguga) sporozoites in accordance with published protocols (Goddeeris & Morrison, 1988). Infected cell lines were maintained in RPMI-1640 supplemented with 10% Fetaclone II (Hyclone, UK; tested for BVDV & *Mycoplasma spp.*), 100iU/ml Penicillin, 100µg/ml Streptomycin, 50µg/ml
10 Gentamycin, 5×10^{-5} M 2-mercaptoethanol and 2mM L-Glutamine and passaged 1/5 three times a week.

Purification of schizonts

 TpM in log growth phase, were harvested and placed in 50 ml Falcon tubes and spun down at 1500 rpm for 10 minutes at room temperature. The cell pellet was resuspended in 50 ml of
15 plain culture medium (RPMI 1640 with 25mM HEPES) and a cell count was [erformed. The suspensions were spun down again to pellet the cells. The cell pellet was resuspended in the residual medium. The cell suspension was mixed with diluted antibody (anti-class I; IL-A19; dilution 1:500 or IL-A88, dilution 1:100), that had been diluted in plain culture medium to yield a final concentration of 1×10^8 cells per ml. Cell suspensions were then incubated on ice for 30
20 minutes. Excess antibody was removed by washing that entailed adding plain culture medium to 50 ml and centrifuging the suspension at 1000 rpm for 10 minutes at room temperature.

 The cell pellet was resuspended in 2-3 ml of plain culture medium, and freshly thawed rabbit serum (Complement, previously tested for toxicity) was added to a final dilution of 1:3 to 1:5 and to a final concentration of 5×10^7 or 1×10^8 cells per ml. The suspension was Incubated at 37
25 °C for 30-90 minutes either in a water bath with shaking at 15 minutes interval until lysis was indicated to be complete (lysis checked by trypan blue differential staining using microscope). The suspension were spun at low speed (800 rpm) for 3 minutes to remove large cell debris. Then the schizont-rich supernatant was transferred into a fresh tube and centrifuged at 2,500 rpm for 10 minutes at 4 °C. The supernatant was discarded and the schizont-rich pellet was resuspended in 6
30 ml of plain culture medium. Schizonts from host cell debris and nuclei were separated by Percoll gradient centrifugation as described by Baumgartner et al. (Baumgartner *et al.*, 1999).

Isolation of mRNA-poly(A⁺) from schizonts

Poly(A⁺)RNA was isolated from frozen pellets containing approximately 3x10⁹ schizonts (from F100 TpM) using FastTrack 2.0 kit (Invitrogen). Frozen schizont pellets were thawed rapidly at room temperature then resuspended and lysed in 15 ml FastTrack 2.0 lysis buffer. The purification of poly(A⁺)RNA was done following the recommendations of the manufacturer
5 (Invitrogen). The total amount of poly(A⁺)RNA isolated and dissolved in 20 µl of sterile distilled water, as estimated by ethidium-bromide-stained agarose gel, was 2 µg. For subsequent analyses, the 20 µl poly(A⁺)RNA in a microcentrifuge tube was precipitated on dry-ice for 20 minutes after addition of 2 µl of 3 M sodium acetate buffer at pH 5.2, 50 µl of absolute ethanol. The frozen
10 solution was thawed and centrifuged at 14,000 rpm for 15 minutes at 4 °C. The ethanol was removed and the RNA precipitate was resuspended in 1 ml of 70% ethanol and re-centrifuged. After removing the ethanol, the RNA was air-dried at room temperature and re-dissolved in 6 µl of water. It was then used to construct a unidirectional cDNA library using Invitrogen cDNA synthesis kit (Cat. No. 11917-010).

Synthesis of cDNA

15 In a microcentrifuge tube, schizont poly(A⁺)RNA (2 µg in 6 µl water) was mixed with 2 µl (1 µg) of oligo(dT) *Not* I primer-adaptor and incubated at 70 °C for 10 minutes. The mixture was spun down briefly then 4 µl 5x first strand buffer, 2 µl 0.1 M DTT, 1 µl 10 mM dNTPs mix and 1 µl [α-³²P]dCTP (1 µCi/µl) were added, mixed and incubated at 37 °C for 2 minutes. After
20 adding 4µl SuperScript II RT, the reaction was mixed gently and incubated at 37 °C for 1 hour. The reaction was placed on ice. One microlitre was removed and used for the calculation of the first strand cDNA yield. The remaining 19 µl was used for the second strand cDNA synthesis. To the remaining 19 µl first strand cDNA reaction placed on ice, 92 µl H₂O, 30 µl 5x second strand
25 buffer, 3 µl 10 mM dNTP mix, 1 µl *E. coli* DNA ligase (10 U/µl), 4 µl *E. coli* DNA polymerase I (10 U/µl) and 1 µl *E. coli* RNase H (2 U/µl) were added. The reaction was mixed gently, spun down briefly and incubated at 16 °C for 2 hours. Two µl (10 U) T4 DNA polymerase was added to
30 the reaction, mixed and incubated for additional 5 minutes at 16 °C. The reaction was stopped by placing the tube on ice and adding 10 µl 0.5 M EDTA. One hundred and fifty microlitres of phenol-chloroform solution was added to the cDNA reaction, and then the mixture was vortexed thoroughly for 30 seconds and spun in a microcentrifuge at 14,000 rpm for 10 minutes at 4 °C. The top aqueous phase was transferred in a fresh tube and extracted with 150 µl chloroform as above. The top aqueous phase was transferred in a fresh tube to which 75 µl 7.5 M ammonium

acetate and 450 µl absolute ethanol were added and mixed. The tube was immediately centrifuged at 14,000 rpm for 20 minutes at room temperature. The supernatant was carefully removed and the cDNA pellet was gently overlaid with 0.5 ml of 70% ethanol. The tube was centrifuged at 14,000 rpm for 2 minutes at room temperature. The supernatant was removed and the cDNA pellet was
5 air-dried at room temperature and then redissolved in 18 µl H₂O.

Ligation and fractionation of cDNA

The ligation was done using Invitrogen kit. The ligation reaction was prepared by adding to the tube containing the 18 µl of ds-cDNA the following reagents: 10 µl 5x Adapter buffer, 10 µl BstX-I adapter (at 1 µg/µl in H₂O) 7 µl 0.1M DTT and 5 µl T4 DNA ligase. The reaction was mix
10 gently and incubated at 16 °C for 20 hours. The ligation reaction was stopped by incubating the tube at 70 °C for 10 minutes then chilling on ice. To the 50 µl of ligation reaction, the following reagents were added and the mixture incubated at 37 °C for 90 minutes: 30 µl H₂O, 10 µl 10x buffer 3 (15 U/µl, GIBCO). A Sepharose CL-2B gel filtration chromatography was prepared during Not I digestion reaction by washing 4 times with 0.8 ml TEN buffer (TEN buffer = 10 mM
15 Tris-Cl, pH 7.5, 0.1 mM EDTA, 25 mM NaCl). The column is very slow and each wash takes about approx. 20 minutes. Fifty microlitre of H₂O was added to the Not I digestion (final volume: 100 µl) and the reaction was loaded onto the column at the center of the resin. All the flow through in a single 1.5 ml Eppendorf tube labeled tube 1. Then 100 µl of TEN was added onto the column and the flow through collected in a single 1.5 ml Eppendorf tube labeled tube 2. From this
20 step, TEN was added to the resin in fractions of 100 µl and only one drop of the flow through was collected in each tube. Fraction collection was done up to tube 24. Each tubes containing cDNA fractions from chromatography was placed in a counting container (with no scintillation fluid) and counted using the tritium channel of a Beckman counter machine. Fractions representing the first 300 µl and fractions collected after the first 3000 µl were discarded. The remaining were grouped
25 into 4 fractions represented by tubes 7 to 12 (fraction A), tubes 13 and 14 (fraction B), tubes 15 and 16 (fraction C) and tubes 17 and 18 (fraction D). The amount of cDNAs was as followed: fraction A, 13 ng; fraction B, 46 ng, fraction C, 95 ng; and fraction D, 82 ng. Five microlitres of each fraction was run on a 1% agarose gel in 0.5x TAE buffer at 7 V/m. The gel was then incubated in 10% TCA containing 1% NaPPi for 20 minutes. The gel was placed on a piece of
30 Whatman 3M paper and overlaid with a pad of absorbent paper and a 500g weight for 10 minutes. The pad of absorbent paper and weight were removed and the gel was dried in a gel dryer under

vacuum for 20 minutes. The dried gel was exposed to autoradiographic film at -80°C overnight (Figure 1).

Cloning of cDNA into pcDNA3 plasmid vector.

Each of the 4 cDNA fractions was adjusted to 150 μl by adding H_2O and 1 μl (10 μg yeast t-RNA). Then 75 μl of 7.5 M NH_4OAc , followed by 450 μl of ice-cold absolute ethanol were added. The mixture was vortexed thoroughly and immediately centrifuged at room temperature for 20 min at 14,000 rpm. The supernatant was removed carefully (and disposed properly), and then the pellet was overlaid with 0.5 ml of ice-cold 70% ethanol and centrifuged for 2 min at 14,000 rpm. The supernatant was removed carefully (and disposed properly). The cDNA was air-dried at room temperature and re-dissolved in H_2O as follow: fraction A in 14 μl , fraction B in 28 μl , fraction in 70 μl and fraction D in 56 μl . Bacteria *E. coli* DH5 α cells containing expression plasmid pcDNA3 were inoculated in 50 ml of 2x YT medium (tryptic soy broth 16 g/l; yeast extract, 10 g/l; NaCl, 5.0 g/l) containing 100 $\mu\text{g}/\text{ml}$ ampicillin and grown overnight at 37°C with vigorous shaking. Bacteria culture was transferred in a 50 ml Falcon centrifuge tube and the cells were pelleted by centrifugation at 3,000 rpm in a minifuge (Heraeus Christ) for 10 minutes at room temperature. The supernatant was discarded and plasmid DNA was purified from bacteria pellet using the QIAprep miniprep (Qiagen)) DNA purification system. Plasmid DNA was eluted in H_2O . Twenty microgram of plasmid DNA (8 μl) was digested with 15 μl (10 U/ μl) of the restriction enzyme Not I (Promega) in 300 μl reaction mixture containing 1x buffer D (Promega) at 37°C for 3 hours. Complete digestion and linearization of the plasmid were confirmed by running 2 μg (30 μl) of the plasmid on a 0.7% agarose gel. The rest of the Not I reaction mix (270 μl) was mixed with 15 μl of BstX I (10 U/ μl) and 15 μl of water and incubated at 55°C for 3 hours. Then 15 μl of the reaction was checked on a 0.7% agarose gel. The rest of the Not I/BstX I double digested pcDNA3 vector (285 μl) was dephosphorylated with 3 μl (3 U) alkaline phosphatase at 37°C for 2 hours. Digested and dephosphorylated plasmid vector was purified using CHROMA SPIN-1000 column (Clontech). The concentration of the vector was adjusted at 50 $\mu\text{g}/\text{ml}$ in water. 1 μl (50 ng) of pcDNA3 was mixed with 1 μl (1 U) T4 DNA ligase (Promega), 1 μl 10x ligation buffer and 7 μl H_2O and incubated at 16°C for 16 hours. The reaction was stopped by heating at 70°C for 10 minutes. Then 10 μl of H_2O is added to give a final concentration of 2.5 ng/ μl . 40 μl of electro-competent bacteria DH5 α previously prepared and tested for their efficiency were electroporated with 2.5 ng (1 μl) of pcDNA3 at 2.49 kV/25 μF using a cuvette of 0.2 cm electrode (BioRad) cold on ice. The electroporated bacteria were resuspended in 1 ml LB medium, incubated at 37°C for 1

hour and then plated on LB agar plates and incubated overnight at 37 °C. Plasmid vector and ds-cDNAs were mixed in a ratio of 50 ng of vector for 10-20 ng of cDNAs in a 20- μ l ligation reaction containing 4 units of T4 DNA ligase (Promega). Thus the final volume of ligation of different was as follow: 20 μ l for the 13 ng of fraction A, 40 μ l for the 28 ng of fraction B, 100 μ l for the 95 ng of fraction C, and 80 μ l for the 82 ng of fraction D. Fraction E was a control ligation reaction of 40 μ l containing 40 ng pcDNA3 and no ds-cDNAs. The ligation reactions were incubated at 4 °C for 16 hours. Water was added to each ligation mix to a final volume of 150 μ l. Followed by 1 μ l of 10 μ g/ μ l yeast t-RNA. Each ligation was extracted with 150 μ l phenol-chloroform by vortexing for 30 seconds and spinning at 14,000 rpm for 10 minutes at 4 °C. The top aqueous phase was re-extracted with 150 μ l chloroform. The top aqueous phase was transferred in a fresh tube and the DNA was precipitated by adding 0.1 volume of 3 M NaAc, pH 5.2, and 2.5 volumes (375 μ l) of ice-cold absolute ethanol, followed by mixing briefly and incubating for 15 minutes on dry-ice. The tubes were thawed at room temperature and centrifuged at 14,000 rpm for 10 minutes at 4 °C to pellet the DNA. The DNA pellet was washed with 1 ml of 70% ethanol, followed by centrifugation at 14,000 rpm for 5 minutes at 4 °C. The supernatant was removed and the DNA pellet was air-dried at Room temperature and re-dissolved in H₂O as follow: fraction A, 5 μ l; fraction B, 10 μ l; fraction C, 25 μ l; fraction D, 20 μ l; and fraction E, 10 μ l. Frozen electrocompetent DH5 α *E. coli* were thawed on ice and maintained on ice with the cuvettes. In ice-cooled Eppendorf tubes, 2.5 μ l of DNA was mixed with 40 μ l of DH5a and transferred in 0.2 cm electrode cuvette for electroporation at 2.49 kV/25 μ F. Each electroporation was recovered with 1 ml LB and transferred in 12 ml Sterilin tubes, followed by incubation at 37 °C for 1 hour on a shaker at 220 rpm. For fraction A, 2 electroporations were done; 4 for fraction B, 10 for fraction C, 8 for fraction D, and only 1 for the control fraction E. Electroporations from the same fraction were pooled together in one tube, mixed and plated. For plating, 20 μ l of each pool was transferred in a fresh tube containing 100 μ l of LB medium: dilution 1. 10 μ l of dilution 1 was transferred in another fresh tube containing 100 μ l of LB: dilution 2; 10 μ l of dilution 2 was transferred in another fresh tube containing 100 μ l of LB: dilution 3. Dilutions 1, 2 and 3 were plated onto LB agar plate containing ampicillin at 50 μ g/ml for the titration of the library. The rest of each electroporation was plated at 2 ml per LB agar plate of 24x24 cm containing ampicillin at 50 μ g/ml. Plates were incubated overnight at 37°C. Colonies from cultures plated out at low dilutions were counted and the total number of colonies in each fraction calculated a shown in

Table 1.

Fractions	Number of independent colonies
A	200
B	12,800
C	355,000
D	298,000
Total library	666,000

Table 1: Titration of cDNA library. The number of independent colonies in each fraction.

The content of a small tube (50 μ l of bacteria) was resuspended in 950 μ l of LB medium, mixed, diluted 10 fold several times and plated on agar plates containing ampicillin.

After incubation overnight at 37 °C, colonies formed on agar plates were counted and the total number of bacteria in each stabilates was determined.

The quality of the library was assessed as described in Table 2.

	Fraction A	Fraction B	Fraction C	Fraction D
% of colonies containing inserts	100	100	95	85
Size of inserts (kb)	1 - 3	0.4 - 3	0.6 - 2	0.2 - 1.5
% of inserts of <i>T. parva</i> origin*	100	100	100	100

Table 2. Analysis of randomly selected cDNA from each fraction. Plasmid DNA was isolated from 20 cDNA clones from each of the 4 fractions, cut with restriction enzymes Hind III and Xba I and analysed for presence and size of inserts, whose sequences were blasted against non-redundant GenBank and TIGR *T. parva* genome databases (<http://www.tigr.org/tdb/e2k1/tpa1/>). *An additional 120 cDNAs were sequenced and found to be of *T. parva* origin.

Preparation of cDNA pools for immunoscreening with CTL

Pools of 50 as well as pools of 10 bacteria was prepared from fractions B and C followed by plasmid minipreps purification. Aliquots of frozen bacteria in small tubes containing 50 μ l of
5 bacteria were diluted and plated on agar plates to a density of 40 - 60 colonies per 4 - 6 cm^2 and grown overnight at 37°C.

Colonies were scraped from the agar plate in pools of about 50 or 10 colonies and resuspended in 3 - 4 ml LB medium with Ampicillin. Bacteria suspensions were cultivated at 37°C for 3 - 4 hrs with shaking. Then 0.8 ml of each culture was mixed with 0.8 ml LB medium
10 containing 40% glycerol and frozen as a glycerol at -80°C while the remaining was used for plasmid purification. Plasmid DNA was eluted in 200 μ l of water then transferred in a well of a 96 wells microwells plate and stored at -20°C until use. For the transfection each pool of cDNAs was adjusted at 100 ng/ μ l.

Strategy for resolving positive pools to identify cDNA coding for CTL target antigen

15 Competent *E. coli* DH5 α (200 μ l) were transformed with 1 μ l (100 ng) of DNA from the positive pool. The transformation was diluted and plated on agar plates to a density of 2000 colonies per 150 cm^2 and grown overnight at 37°C.

For a positive pool of 10, only 48 individual colonies were picked and grown overnight in 2 ml of 2x YT medium containing ampicillin. Plasmid DNA was then isolated from each bacteria culture
20 by minipreps. Plasmid DNA were eluted in 200 μ l of water and then transferred in a well of a 96 wells microwells plate and stored at -20 °C. The working concentration was adjusted at 100 ng/ μ l and stored at -20 °C until use. For a positive pool of 50, a three-way matrix was used as follow:
256 individual colonies were picked and seeded in 200 μ l of 2x YT medium containing ampicillin in 4 flat-bottom microwells plates. This gave 64 colonies per plate. Bacteria were grown at 37 °C
25 overnight. From each plate containing 64 cultures, 12 pools of bacteria, each containing 16 individual bacteria cultures, were prepared by pooling 50 μ l of each individual bacteria culture as shown in the table 3 below. In total, 48 pools of 16 individual bacteria were generated. Glycerol was added to 20% in the each of the remaining cultures in Table 3 and stored at -70 °C until the results of the screening allowed the picking of the positive colonies.

Use of a 3-way matrix for rapid recovery of a positive cDNA clone

Competent *E. coli* cells (200 μ l) were transformed with 1 μ l (100 ng) of DNA from the positive pool of 50 cDNAs. Transformed *E. coli* were diluted and plated on agar plates to a density of 2000 colonies per 150 cm² and grown overnight at 37°C. Two hundred fifty six (approximately 5x coverage of 50 cDNA per positive pool) individual colonies were picked and seeded in 200 μ l of 2x YT medium containing ampicillin in 4 flat-bottom microwells plates to have 64 single bacteria colony cultures per plate arrayed in a 8 x 8 format and numbered from 1 to 64 as tabulated below (this is one of 4 plates containing 64 *E. coli* cultures).

		1	9	17	25	33	41	49	57		
		2	10	18	26	34	42	50	58		
		3	11	19	27	35	43	51	59		
		4	12	20	28	36	44	52	60		
		5	13	21	29	37	45	53	61		
		6	14	22	30	38	46	54	62		
		7	15	23	31	38	47	55	63		
		8	16	24	32	40	48	56	64		

Twelve pools of 16 individual cultures were generated from the 4 plates as shown in the table below. This format was high throughput in that use of a multi-channel pipetting device, accelerated the process. The 3-way matrix was such that each individual bacteria culture was present in 3 pools. Pools of bacteria cultures were grown at 37°C for 3 hours with shaking before plasmid DNA was extracted from pooled 16 aliquots of each pool. Glycerol was added to the remaining cultures in microplates and stored at -70°C. Plasmid DNA was adjusted at 100 ng/ μ l and used for transfection in screening assays. A positive cDNA clone was detected in 3 pools. For example, colony #25 contained the target cDNA clone, so pools #2, 5 and 11 were positive. Plasmid DNA was then prepared from the glycerol stock of bacteria colony #25 from the 3 pools individually and re-tested and sequenced.

	Pool 1	Pool 2	Pool 3	Pool 4	Pool 5	Pool 6	Pool 7	Pool 8	Pool 9	Pool 10	Pool 11	Pool 12
Colony #	1	17	33	49	1	2	3	4	1	5	9	13
	2	18	34	50	5	6	7	8	2	6	10	14
	3	19	35	51	9	10	11	12	3	7	11	15
	4	20	36	52	13	14	15	16	4	8	12	16
	5	21	37	53	17	18	19	20	17	21	25	29
	6	22	38	54	21	22	23	24	18	22	26	30
	7	23	39	55	25	26	27	28	19	23	27	31
	8	24	40	56	29	30	31	32	20	24	28	32
	9	25	41	57	33	34	35	36	33	37	41	45
	10	26	42	58	37	38	39	40	34	38	42	46
	11	27	43	59	41	42	43	44	35	39	43	47
	12	28	44	60	45	46	47	48	36	40	44	48
	13	29	45	61	49	50	51	52	49	53	57	61
	14	30	46	62	53	54	55	56	50	54	58	62
	15	31	47	63	57	58	59	60	51	55	59	63
	16	32	48	64	61	62	63	64	52	56	60	64

Table 3: A 3-way matrix for rapid resolution of positive pools. In this format each colony is represented three times.

- 5 Pools of bacteria were grown at 37 °C for 3 hours with shaking before they were used for plasmid purification by minipreps. Plasmid DNA were eluted in 200 µl of water and then transferred in a well of a 96 wells microwells plate and stored at -20 °C. The working concentration was adjusted at 100 ng/µl and stored at -20 °C until use.

Immunisation & details of cattle

- 10 The 7 cattle used in this invention were pure bred *Bos indicus* (Boran) pure bred *Bos taurus* (Friesian) or crossbreeds. Cattle were immunised by 'infection and treatment' against the Muguga stock of *T. parva* by simultaneous inoculation of sporozoites and long-acting oxytetracycline at 20mg/kg BW (Radley et al 1975). Cryopreserved sporozoites (Stabilate # 4133) were thawed and diluted 1/20 as previously described. Animals were given a subcutaneous
- 15 injection of 1ml of diluted sporozoites 2cm above the right parotid lymph node. Animals were monitored daily for changes in rectal temperature and from day 5 post challenge lymph node biopsies were taken using a 21G needle. Giemsa stained biopsy smears were examined for the

presence of schizont infected cells and scored on a scale of 1-3. Animals suffering from moderate reactions were treated with Buparvaquone (Butalex, Mallinckrodt Veterinary Ltd, UK).

Establishment of TpM

Prior to immunisation, venous blood was collected from the eleven animals, PBMC were
5 purified and infected *in vitro* with *T. parva* (Muguga) sporozoites (Goddeeris & Morrison, 1988).

Generation of *T. parva* specific CD8⁺ CTL

Venous blood from immunised animals was collected from 4 weeks post-immunisation. PBMC were prepared as described previously (Goddeeris & Morrison, 1988). PBMC were adjusted to 4×10^6 /ml in CTL medium (RPMI-1640 without HEPES supplemented with 10% FBS
10 (HyClone; tested for BVDV & mycoplasma spp.), L-glutamine, 2-mercaptoethanol and antibiotics as described above) and 1ml/well added to 24 well plates (Costar, Corning, NY, USA). PBMC were co-cultured with irradiated (50Gy) autologous *T. parva* infected cells (TpM) at 2×10^5 /well and incubated for 7 days at 37°C in a 5% CO₂ humidified atmosphere. Cells were harvested by aspiration and dead cells removed by centrifugation over Ficoll-Paque Plus (Amersham Pharmacia
15 Biotech, Uppsala, Sweden). After washing in CTL medium, cells were added to 24 well plates (3×10^6 /well) and co-cultured with irradiated PBMC (filler cells) at 1×10^6 /well and TpM at 2×10^5 /well for 7 days as before. Viable cells were harvested as described above, adjusted to 2×10^6 /well and stimulated with 4×10^5 /well irradiated TpM and 2×10^6 /well irradiated autologous PBMC as filler cells.

20 ⁵¹**Chromium Release Assay:** Autologous and allogeneic TpM in log phase of growth were resuspended at 2×10^7 /ml cytotoxicity medium (RPMI-1640 medium with 5% Fetaclone II). 100μl of the target cells were mixed with 100μl (100μCi) of ⁵¹Cr-sodium chromate and incubated for 1 hour at 37°C. Cells were washed 3 times in 7ml of cytotoxicity medium by centrifugation at 1500 rpm for 7 min at RT and resuspended at 1×10^6 /ml. Viable cells were harvested from TpM
25 stimulated lines 7 days post-stimulation (effector cells) and resuspended in cytotoxicity medium at 2×10^7 /ml. Two-fold doubling dilutions of effector cells were distributed in duplicate (100μl/well) to 96-well half area (A/2) flat-bottom culture plates (Costar, Corning, NY, USA) resulting in a range of effector cell concentrations of 4×10^6 to 2.5×10^5 /well. Target cells were added to each well containing effector cells (50μl/well) resulting in target cell ratios ranging from 80:1 to 5:1. In
30 separate triplicate wells target cells were added to 100μl cytotoxicity medium or 1% Tween20 to measure spontaneous and maximal release of the label respectively. Plates were incubated for 4 hours at 37°C in 5% CO₂ humidified atmosphere. Cells were resuspended in wells by repeated

pipetting and pelleted by centrifugation at 180Xg at room temperature. 75 μ l of supernatant was transferred from each well into sample vials (Milian, Geneva, Switzerland) and gamma emissions counted in a gamma counter (Micromedic MEplus, TiterTek, Huntsville, AL, USA). Results were calculated and expressed as percent cytotoxicity (= 100 x (test release – spontaneous release) / (maximum release – spontaneous release)).

Evidence for MHC class I restricted lysis was assessed by the capacity of monoclonal antibodies recognising bovine MHC class I to inhibit lysis. Cells were prepared for the cytotoxicity assay as described above except that target cells were resuspended at double the density (2x10⁶/ml) and 25 μ l added first to the plate. 25 μ l of either cytotoxicity medium or monoclonal antibody (mAb; IL-A88 diluted 1/15 in cytotoxicity medium was added to target cells and incubated for 30min at room temperature. Serial dilutions of effector cells were then added as described above.

Viable cells from TpM stimulated cultures were harvested day 7 post-infection and CD8⁺ T cells were isolated either by positive selection using flow cytometry (FACStar Plus, BD Biosciences, San Jose, CA, USA) or negative selection using Dynabeads (DynaL Biotech, Bromborough, UK).

Positive selection: Cells were adjusted to 2x10⁷/ml in sterile monoclonal antibody IL-A105 (specific for bovine CD8) diluted 1/100 and incubated for 30 minutes at 4°C. Cells were washed twice in cold culture medium and resuspended at 2x10⁷/ml in sterile goat anti-mouse polyvalent immunoglobulins conjugated to FITC (Sigma). Cells were washed twice in cold medium before being run through a FACStar plus cell-sorter and CD8⁺FITC⁺ cells collected.

Negative selection: Cells were adjusted to 2x10⁷/ml in sterile mAbs IL-A12 (specific for bovine CD4) and GB21A (specific for bovine $\gamma\delta$ TCR) diluted 1/100 and incubated for 30 minutes at 4°C. Cells were washed twice in cold PBS and resuspended 1.4x10⁷/ml in sterile PBS containing washed sheep anti-mouse IgG Dynabeads according to the manufacturers instructions. Cells and beads were rotated for 30 min at 4°C and Dynabead rosetted cells were collected by placing the sample tube in a Dynal Magnetic Particle Concentrator (MPC) for 5 min, the supernatant was removed, transferred to another sample tube and residual Dynabead rosetted cells removed by another incubation in a Dynal MPC. The supernatant was removed and cells washed twice in complete medium.

Cloning: CD8⁺ T cells enriched by either of the methods described above were adjusted to 30, 10, and 3 cell/ml and distributed into 96-well, round bottom culture plates containing 2 x 10⁴ irradiated autologous TpM, 5 x 10³ irradiated autologous PBMC and 5U/ml recombinant human

IL-2 (HuIL-2; Sigma, Poole, UK) in a final volume of 200 μ l/well. Plates were incubated at 37°C in humidified incubator containing 5% CO₂ in air. Wells showing significant cell growth were selected for analysis of lysis of autologous TpM in an (¹¹¹In) Indium oxine release assay. The ¹¹¹In release assay was performed as described above for ⁵¹Cr release assay except that targets cells were
5 labelled by addition of 5 μ Ci ¹¹¹In/1 x 10⁶ cells and incubation for 15 minutes at 37°C. Cells were washed five times with cytotoxicity medium and resuspended at 1x10⁵/ml and added 50 μ l/well to 96-well V-bottom 96 well plates. 100 μ l cells from wells showing significant growth were transferred to 96-well V-bottom culture plates (Greiner) and centrifuged (180xg) for 5 min. Cells were resuspended 100 μ l/well in cytotoxicity medium and transferred to wells containing labelled
10 target cells. Plates were centrifuged as described above to pellet cells before being incubated for 4 hours at 37°C in 5% CO₂ humidified atmosphere.

CTL populations that exhibited lytic activity on autologous infected cells and originated from cell dilutions that gave rise to cell growth in less than 30% of the wells, as they have high probability of being clones, were selected for expansion. The remaining cells were harvested from
15 each well and resuspend them in culture medium (without HEPES) at a concentration estimated to be between 500 and 5000 cells/ml. 100 μ l of cell suspension was distributed into 96 well, round bottom culture plates. 100 μ l of autologous irradiated TpM at 5 x10⁴ autologous irradiated TpM in medium containing 5U/ml HuIL-2. Between day 14 and 21 post-stimulation clones and polyclonal CTL lines were subcultured in 96 well, round bottom culture plates by co-culturing 5000 CTL/well
20 with 25,000 autologous irradiated TpM and 5U/ml HuIL-2 in a final volume of 200 μ l/well.

Establishment and maintenance of bovine skin fibroblasts

A skin biopsy was taken aseptically from the ears of cattle and placed in a 50ml falcon tube containing Alsever's solution. In the laboratory laminar flow hood, the biopsy was placed into sterile petri dishes (Sterilin) containing 1ml of 0.25% Trypsin-EDTA. Using a sterile scalpel blade,
25 the sample was cut into small pieces and placed into a 50 ml falcon tube containing Trypsin-EDTA. The preparation was placed in a shaking incubator for 1-1.5 hr at 37°C with gentle continuous shaking. This facilitates detachment of cells. This digestion was stopped by addition of 1ml heat-inactivated FBS. The cell suspension was centrifuged for 10 min at 200xg and the cell pellet re-suspended in 6 ml of Dulbecco's minimum essential medium, DMEM (Gibco-BRL,
30 Paisley, UK) supplemented with 10% heat-inactivated fetal bovine serum (FBS) (Hyclone, Logan, UT), 400 IU/ml penicillin, 300 μ g/ml streptomycin and 2 mM L-glutamine. This cell suspension was seeded in 5ml amounts into 25-cm² flasks and incubated at 37°C in a 5% CO₂ humidified

atmosphere. Cultures were examined microscopically after every 4 days for growth and half the medium was replaced with fresh one until growing colonies were evident. Once positive colonies were identified they were rinsed with Ca^{2+} - and Mg^{2+} -free PBS/EDTA (0.02% EDTA) and detached by 2 min incubation at 37°C with Trypsin-EDTA solution containing 2.5 mg/ml Trypsin and 0.2 mg/ml EDTA in HBSS (Sigma). Following a wash in complete DMEM containing 10% FBS the skin fibroblasts (SF) were passaged into 25-cm² tissue culture flasks (Costar). Cells were maintained in complete DMEM containing 10% FBS, 200 IU/ml penicillin, 100 µg/ml streptomycin and 2 mM L-glutamine and passaged every 3 days at a ratio of 1:3. Cells were expanded in 75-cm² tissue culture flasks (Costar) until confluent yielding 3-4×10⁶ cells/flask. For consistency a liquid nitrogen cell bank was prepared with 2×10⁶ cells/freezing vial in 10% DMSO in FBS.

Establishment and maintenance of bovine testicular endothelial cells

Bovine testicular vein or pulmonary artery EC lines were established as described by Byrom and Yunker (1990) with the modifications of Mwangi et al (1998). Briefly, the vein was placed in wash buffer consisting of Ca^{2+} - and Mg^{2+} -free PBS supplemented with 400 IU/ml penicillin, 400 µg/ml streptomycin and 5 µg/ml fungizone. The vessel was then slit longitudinally, washed twice before being cut into 1-cm² pieces and then placed lumen side down on a drop of collagenase (1 mg/ml) and incubated for 1 h at 37°C. The cell suspension was centrifuged for 5 min at 200×g and re-suspended in 24 ml 2× complete DMEM (Gibco-BRL, Paisley, UK) supplemented with 20% heat-inactivated fetal bovine serum (FBS) (Hyclone, Logan, UT), 400 IU/ml penicillin, 300 µg/ml streptomycin, 5 mg/ml fungizone, 300 µg/ml endothelial growth supplement (Sigma, St Louis, MO) and 2 mM L-glutamine. One ml of the cell suspension was seeded in each well of a 24-well tissue culture plate (Costar, Cambridge, MA, USA). Once confluent, monolayers in each well were rinsed with Ca^{2+} - and Mg^{2+} -free PBS/EDTA (0.02% EDTA) and detached by 2 min incubation at 37°C with 0.25% trypsin/EDTA solution containing 2.5mg/ml trypsin and 0.2 mg/ml EDTA in HBSS (Sigma). Following a wash in DMEM containing 10% FBS the cells were passaged into 25-cm² tissue culture flasks (Costar). Cells were maintained in complete DMEM containing 10% FBS, 200 IU/ml penicillin, 100 µg/ml streptomycin, 2.5 mg/ml fungizone, 2 mM L-glutamine and passaged every 3 days at a ratio of 1:3. Cells were expanded in 75-cm² tissue culture flasks (Costar) until confluent yielding between 3×10⁶ and 4×10⁶ cells per flask. For consistency a liquid nitrogen cell

bank was prepared with 2×10^6 cells per freezing vial. Cells were raised from nitrogen into 75-cm² flasks and used between the fourth and tenth passages.

Immortalization of bovine skin fibroblasts and endothelial cells

Cells were immortalized with the SV40 early region gene by transfection of an
5 expression plasmid psvNeo (ATCC code 37150). The product is supplied as a freeze dried to which 300ul of 2XYT with ampicillin was added and fully resuspended. The 300ul suspension was sub-cultured into 6mls and divided into 3mls each. The cultures were incubated overnight at 37°C and then subcultured again into 50mls of 2XYT with ampicillin overnight at 37°C. Maxiprep of psvNeo plasmid were made for use in immortalizations. Plasmid DNA for transfection was
10 standardized to 2mg/ml.

The DNA mix was prepared by mixing 5μl DNA with 495μl of DMEM with antibiotics but no serum. A working dilution of Fugene 6 transfection reagent (Roche) was prepared by mixing 15μl of Fugene with 485μl of DMEM. Mixing was done using the 2ml sterile non-pyrogenic, DNase and RNase free cryopreservation tubes. The diluted Fugene was added to the
15 diluted DNA drop wise with constant tapping at the end of the tube. The Fugene-DNA complex was allowed to form at room temperature for 30 min.

Cells were cultured in 6-well plates (Costar) at a density of 2×10^5 cells per well and grown to confluence overnight at 37°C, 5% CO₂ in a humidified incubator. Culture medium was removed completely from the monolayers to be transfected. The Fugene-DNA complex was then
20 added gently onto the monolayer. Plates were incubated at 37°C, 5% CO₂ in a humidified atmosphere for 3-4 hours. The transfection complex was removed; fresh DMEM medium containing 10% fetal calf serum was added and then cultured for a further 72h. Cells from each well were rinsed with PBS/EDTA, detached with Trypsin/EDTA, washed and re-suspended in complete DMEM and sub-cultured into one T-25 flask (Costar). After incubation for 2-3h, normal
25 DMEM medium was removed and replaced with a selection DMEM medium containing 10% FCS and 0.5μg/ml of G418 (2.5μg/ml G418 for endothelial cells) and incubated further. Upon observation of high death rate of cells, half the medium was replaced with fresh selection medium until growing colonies were evident. This process took 3-4 weeks depending on the cell lines. Positive colonies were the sub-cultured into 24 well plates and then to T-25 flasks. Immortalization
30 was confirmed by checking for expression of large T-antigen using an anti-SV40 antibody conjugated to HRP. Further expansion and maintenance of the cells was carried out using complete DMEM.

Transfection of COS-7 cells and immortalised skin fibroblasts with schizont cDNA library

COS-7 cells and iSF were maintained in T75 and T150 TC flasks with DMEM supplemented with 10% FCS, 2mM L-glutamine and antibiotics (TC medium) as described above. Cells are split 1:4 every 3 days. The day prior to transfection, cells were harvested by the removal of medium, washing in PBS and incubation in 0.25% Trypsin-EDTA for 5 min at 37°C. Once cells had detached TC medium was added and cells removed. Cells were washed by centrifugation at 1200 rpm for 10min and resuspended in TC medium. A viable cell count taken, density adjusted to 2.0×10^5 /ml, cells dispensed, 100 μ l/well, into 96 well flat-bottom TC plates and incubated for overnight at 37°C in a CO₂ (5%) humidified incubator.

DNA was prepared for either single transfections of SF or double transfections (co-transfection of schizont cDNA and BoLA class I cDNA) of COS cells. 6 μ l of schizont cDNA and 6 μ l of BoLA class I cDNA (for co-transfection) at 50ng/ μ l in dH₂O were added to 150 μ l unsupplemented DMEM in wells of a 96-well round-bottom plate. FuGENE 6 transfection reagent was pre-warmed to 37°C. 0.9 μ l or 0.45 μ l FuGENE 6 was added to each well for double and single transfections respectively. The well contents mixed by shaking on a Dynatech Varishaker for 1 min and incubated at RT for 20 min. The medium from the 96 well plates containing adherent COS cells and SF was removed and each transfection complex added to triplicate wells (50 μ l/well). The cells were then incubated for 4 hours at 37°C in a CO₂ (5%) humidified incubator. The transfection complex was removed and replaced with 200 μ l/well DMEM supplemented as described above and incubate for 24 or 48 hours at 37°C in a CO₂ (5%) humidified incubator.

Detection of CTL recognition of transfected SF and COS-7 cells by**IFN-gamma ELISpot**

24 hours post-transfection, medium was removed from wells containing transfected cells, cells were washed cells with PBS (200 μ l/well) and detached by the addition of 100 μ l/well Trypsin-EDTA as described above. Once the cells had detached the contents of each well were transferred to a 96 well round-bottom plates containing 100 μ l/well cold RPMI with no HEPES supplemented with 10% FCS (CTL medium). The cells were centrifuged at 1200 rpm for 3 min; supernatant removed and resuspended 50 μ l/well in CTL medium Schizont specific CTL, generated and maintained as described above, were harvested 7-14 days post-stimulation, transferred to polycarbonate tubes, pelleted at 1200 rpm for 10min and resuspended at 2×10^5 /ml in CTL medium supplemented with 5U/ml HuIL-2 (Sigma).

ELISpot plates (Millipore corporation, Bedford, MA, USA) were coated 50 μ l/well with 2 μ g/ml of murine anti-bovine IFN- γ mAb (CC302; Serotec, UK) and incubated overnight at 4°C. Wells were washed twice with unsupplemented RPMI-1640 and blocked 200 μ l/well with RPMI-1640 supplemented with 10% FBS by incubating at 37°C for 2 hours. The blocking medium was removed and replaced with 50 μ l/well CTL and 100 μ l/well transfected cells. As a positive control, irradiated TpM are serially diluted in COS cells or SF with each at a density of 4x10⁵/ml. and populations containing 32, 16, 8, 4, 2, 1% TpM are added 50 μ l/well to wells containing CTL. Plates were incubated in a humidified incubator at 37°C for 20 hours. After incubation, the contents of wells were removed and wells washed four times with sterile distilled water supplemented with 0.05% Tween 20 per well and the plate shaken on a shaker for 30 seconds between washes. The process was repeated an additional four times, using PBS supplemented with Tween 20 (PBS-T). Wells were then incubated with 100 μ l/well rabbit anti-bovine IFN- γ antisera diluted 1/1500 in PBS-T supplemented with 0.2% BSA (PBS/BSA) for 1 hour at room temperature. Wells were washed 4 times with PBS-T before being incubated for 1 hour at room temperature with 100 μ l/well murine monoclonal anti-rabbit IgG conjugated to alkaline phosphatase (Sigma) diluted 1/2000 in PBS-T/BSA. Sigma Fast BCIP/NBT buffered substrate (Sigma) was by dissolving 1 tablet/10ml dH₂O and passing it through a 0.2 μ m filter. Plates were washed six times as described above with PBS-T, 100 μ l/well BCIP/NBT substrate added and plates incubated for 10 minutes at room temperature in the dark. The substrate was then removed, wells washed with copious amounts of H₂O and plates air-dried at room temperature in the dark. Plates were finally read on an automated ELISpot reader (AID Diagnostica, Strasberg, Germany).

Bioassay for CTL activation based on rapid induction of class II MHC expression by constitutively negative bovine endothelial cells

Endothelial cells were detached from confluent 75-cm² tissue culture flasks by treatment with trypsin/EDTA as described. 2.5x10⁴ cells were seeded into each well of a 48-well plate in 1 ml of complete DMEM and incubated overnight. Cell-free test supernatants derived from either co-culture of *T. parva*-specific CD8⁺ T cell lines and SF transfected with test genes or recombinant bovine IFN- γ (rBoIFN- γ , the kind gift of Ciba-Geigy, Basel, Switzerland) were dispensed in duplicate wells in a final volume of 160 μ l per well. Following 48 h at 37°C, culture supernatants were discarded and the monolayers were washed 3X in FACS medium (RPMI 1640 supplemented with 2%-globulin-free horse serum and 0.1% sodium azide). Endothelial cells are labelled on ice for 30 min with 100 μ l of an antibody cocktail comprising equal volumes of bovine class II MHC-

specific monoclonal antibodies (mAbs) J11, R1, and IL-A21 (each at a 1/500 dilution of ascitic fluid). After 3 washes in FACS medium, 100 μ l of FITC-conjugated goat anti-mouse Ig (Sigma) diluted 1/200 in FACS medium were added. After incubation at 4°C for 30 min and a further three washes in FACS medium, cells were detached as described previously and cell surface class II MHC expression determined by flow cytometry, using a FACScan (Becton-Dickinson, Sunnyvale, CA, USA). The percentage of class II MHC-expressing cells was determined by comparison with unstimulated EC labeled in an identical manner.

T. parva-specific CD8⁺ CTL lines were generated and maintained using methods initially described. Test supernatants were collected from 96-well flat-bottomed microtitre plates (Costar) 48 hours after restimulation of resting T cell lines (2×10^4 per well) with 4×10^5 COS-7 cells co-transfected with the KN104 gene and test gene(s) or confluent autologous SF transfected with the test gene(s) in a final volume of 200 μ l for 24 h. These tests were set-up at least in duplicates. Where indicated, class I MHC was blocked using a specific antibody (IL-A88) to check for MHC class I restriction of the CTL lines. Additional negative control supernatants were derived from co-culture of CTL with untransfected immortalized SF or COS-7 cells. Positive control supernatants were obtained from co-culture of CTL with varying proportions of irradiated autologous TpM.

Detection of CTL lysis of transfected iSF and COS-7 cells

Autologous iSF or COS-7 cells were seeded in 6-well plates (Costar) at a density of 2.5×10^5 /well and incubated for 2 hours at 37°C to allow cells to adhere. For single transfections of iSF, 2 μ g of test or control cDNA was added to 1ml unsupplemented DMEM containing 3 μ l FuGENE 6 transfection reagent and incubated for 40min. For COS-7 cells, 2 μ g of test or control cDNA was added with 2 μ g of BoLA class I cDNA to 1ml DMEM containing 6 μ l FuGENE. 1ml of DNA/Fugene complex was added per well of adherent COS-7 or iSF. Plates were incubated for 4 hours at 37°C; the transfection complex was removed and replaced with 2ml/well of complete DMEM and the plates incubated for a further 20 hours at 37°C. Transfected cells were harvested by removal of medium, washing in PBS, detachment by Trypsin-EDTA and washing in complete DMEM. Transfected cells and TpM were labelled with ⁵¹Chromium and the ability of schizont-specific CTL lines (day 6-8 post-stimulation) to lyse these targets was assessed as described above.

Use of Exonuclease III digestion to map epitope-encoding regions from Tp1

The recombinant Tp1 plasmid DNA was cut with restriction enzyme Apa I to generate Exonuclease III resistant 3'-protruding termini. The linearized plasmid DNA was then purified with phenol-chloroform before digestion with the restriction enzyme Xho I that will cut at the

single and unique vector cloning site Xho I located between Not I and Apa I sites (NB: the Tp1 cDNA insert does not contain neither Apa I nor Xho I sites). Digestion of the DNA with Xho I generated an exonuclease III sensitive recessed 3'-terminus (only at the 3' side of the cDNA insert). The linearized plasmid DNA was purified as described previously, 100 µg of DNA was digested at 5 37 °C with 1 unit of Exonuclease III in 20 µul reactions at varying times (from 0 to 30 minutes). Reactions were stopped by 10 minutes incubation at 75 °C, DNA was ethanol-precipitated, washed with 70% ethanol, air-dried and re-dissolved in 20 µul of 1x Mung Bean nuclease. Five units of Mung Bean nuclease were added to each reaction, mixed and incubated at 30 °C for 1 hour to remove single-stranded extensions and create ligatable blunt ends. The DNA was again purified 10 with phenol-chloroform, precipitated with ethanol, washed with 70% ethanol, air-dried and re-dissolved in 10µl of sterile distilled water. For re-ligation, 5µul of DNA was mixed with 1µul of 10x T4 ligation buffer, 3µl of water and 1µl of T4 DNA ligase, and incubated at 16 °C overnight. Competent *E. coli* DH5α was transformed with 2 µl of the ligation and plated on agar plates as previously described. Plasmid DNA was isolated from single bacteria colonies as described and the 15 inserts were excised by double digestion with BamH I and Bbs I (an isoschizomer of Bbv II). Plasmid clones with different cDNA inserts were selected for IFN-γ ELISpot screening. Oligonucleotide primers were generated and used in PCR to clone small overlapping fragments of a 600 bp region containing the CTGAMMA epitope, into the mammalian expression plasmid vector pTargetT (Promega). Clones generated were then analysed by IFN-GAMMAγ ELISpot.

20 Identification of Tp1 CTL epitopes with synthetic peptide libraries

Peptide libraries (Cleaved PepSets; Mimotopes, Clayton, Australia) were generated for the 66 amino acid portion of Tp1 shown to contain the HD6 restricted CTL epitope. The PepSet libraries contained every 12mer, 11mer, 10mer and 9mer offset by 2 amino acids from the protein sequences. However, the peptides were prepared by truncations of the 12mers at the N-terminus 25 and were supplied lyophilised with each tube containing a nominal 12mer and the 9, 10, 11mer truncations with the same C-terminus. Peptides were dissolved in 400µul 50% (v/v) DNA synthesis grade acetonitrile/water (Applied Biosystems, Warrington, UK). To aid the dissolution, tubes were held in a sonicator water bath for 2 x 10 min. Peptides were aliquoted into labelled cryopreservation tubes (Greiner) and stored at -20°C. For screening with CTL, peptides were 30 prepared at 10µg/ml in complete RPMI-1640 and 10µul added to triplicate wells of an ELISpot plate, coated, washed and blocked as described above. Autologous iSF or P815 cells stably

expressing the BoLA class I HD6 (P815-HD6) or JSP-1 (P815-JSP-1) were adjusted to a density of 4×10^5 /ml and 50 μ l added to wells containing peptides. The plates were incubated at 37°C for 1 hour before CTL, prepared as described above for screening transfectants, were added 50 μ l/well. Plates were incubated for 20 hours at 37°C and then developed as described above. Based on the results of the screening with the Tp1 PepSet, individual 9, 10 and 11mer peptides were synthesised in order to define the CTL epitopes. Peptides were prepared and screened using the IFN- γ ELISpot as described above.

Peptide-pulsed iSF and BoLA class I P815 transfectants were prepared as targets for 51 Chromium release assays by incubating 2×10^6 iSF or P815 cells overnight in T25 tissue culture flasks (Costar) with Tp1 peptides diluted to 1 μ g/ml in complete DMEM. Cells were harvested, labelled and assayed as described above.

Detection of Tp1 specific *ex vivo* CD8⁺ T cell responses from immune cattle after challenge with *T. parva* sporozoites

Bull BV115, whose schizont specific CTL lines had been shown to recognise Tp1, was challenged with a lethal dose of *T. parva* (Muguga) sporozoites. Cryopreserved sporozoites (Stabilate # 4133) were thawed and diluted 1/20 as previously described. Animals were challenged by subcutaneous injection of 1ml of diluted sporozoites 2cm above the right parotid lymph node. Animals were monitored daily for changes in rectal temperature and from day 5 post challenge lymph node biopsies were taken using a 21G needle. Giemsa stained biopsy smears were examined for the presence of schizont infected cells and scored on a scale of 1-3. Animals were bled on day 0 and daily from day 6 to 13 and PBMC were isolated as described above. CD8⁺ T cells and CD14⁺ monocytes were purified from PBMC by MACS magnetic cell sorting according to the manufacturers instructions (Miltenyi Biotec, Gergisch Gladbach, Germany). CD8⁺ T cells were sorted indirectly using a monoclonal antibody specific for bovine CD8 (IL-A105) followed by incubation with goat anti-mouse IgG microbeads (Miltenyi Biotec). CD14 monocytes were sorted directly by incubation with CD14 microbeads (Miltenyi Biotec). PBMC and CD8⁺ T cells were added to wells (2.5×10^5 /well) of coated/blocked ELISpot plates and stimulated with autologous TpM (2.5×10^4 /well) or Tp1 peptides (1 μ g/ml final concentration). Purified monocytes were additionally added (2.5×10^4 /well) to wells containing peptide and CD8⁺ T cells. ELISpot plates were incubated and developed as described above.

In order to recall Tp1 peptide specific CTL responses, PBMC were stimulated with autologous TpM 14 days post-challenge as described above. Viable cells were harvested 7 days post-

stimulation and lytic activity against TpM and Tp1 peptide pulsed uninfected T cell blasts assessed as described above.

Results of screening for CTL target antigens

Optimisation of INF-gamma ELISpot for the recognition of target antigens by schizont specific CTL

The ability of the IFN-GAMMA- γ ELISpot to detect the recognition of TpM by CTL was first assessed using a CD8⁺ polyclonal CTL line from animal F100. Fourteen days post-stimulation, CTL were added (5000/well) to coated/blocked ELISpot wells containing 25,000 irradiated autologous schizont and the formation of IFN-GAMMA- γ spots assessed after a 20-hour incubation. CO-culture of CTL with TpM resulted in significant release of IFN-GAMMA-gamma. Pre-incubating the CTL for 30 min with a mAb against BoLA class I completely inhibited the IFN-GAMMA- γ response whilst mAbs against MHC class II or the irrelevant CD21 antigen had no effect. Significantly, there was almost no spontaneous release of IFN-GAMMA- γ from CTL cultured without TpM. This TpM line did not constitutively express TpM and no IFN-GAMMA- γ spots could be attributed to the TpM.

In an attempt to replicate the transient transfection situation, where CTL would be co-cultured with COS-7 or iSF of which only a small proportion of cells would be expressing the target antigen, TpM were titrated in COS-7 or iSF and co-cultured with CTL in IFN-GAMMA- γ ELISpot plates. The stimulator population was fixed at an input of 40,000/well, with only the proportions of TpM and COS-7/iSF varying. This cell input was adopted since it was thought to mirror the numbers of APC that would be co-cultured with CTL after transient transfection. Initially different CTL inputs were tried against TpM titrations with the aim of identifying the minimum CTL input required to detect significant responses to 1-3% TpM. A CTL input of 10,000/well was determined to be optimal since it could elicit significant responses to less than 1% TpM and it was practically feasible to raise such CTL numbers for screening experiments. Further titration experiments were performed with CTL clones from F100 to confirm that with these CTL and APC inputs the IFN-GAMMA- γ ELISpot was meeting or exceeding the desired sensitivity level. With all the clones tested the IFN-GAMMA- γ ELISpot could still detect recognition of target cells when they constituted only 0.1% of the total cell population. The ELISpot assay worked well with little background noise and met the sensitivity requirements when TpM were titrated in COS-7 cells but it was important to determine that the assay performed as well when the

TpM were titrated in autologous SF. Neither primary nor iSF significantly affected the background levels or the sensitivity of the ELISpot assay.

In advance of the initiation of screening for CTL target antigens by the transient transfection of COS-7 cells and iSF, the efficiencies of COS-7 and iSF transfection in 96 well TC plates was assessed using GFP as a reporter gene. Whilst there was considerable variation in transfection efficiencies between cell lines and between experiments, COS-7 consistently transfected better than iSF with efficiencies varying from 5-50% whereas for iSF transfection efficiency ranged between 0.5 – 20%. The transfection efficiency of iSF was assessed to be good enough to allow the presentation and identification of transfected schizont cDNA.

10 **Evaluation of IFN-GAMMA- γ Bioassay as a complementary read-out system for CTL recognition of target antigens**

Bovine vascular EC were stained for surface class II MHC expression following culture for 48 h in the presence of media containing recombinant IFN-GAMMA- γ . The sensitivity to rBoIFN-gamma was determined and found to be between 100 and 10 pg/ml. Comparisons were made between IFN-GAMMA- γ bioassay and ELISpot by co-culturing *T.parva*-specific CTL with fixed number of autologous iSF containing varying proportions of target autologous TpM and skin fibroblasts. There was a good correlation between the two assays. Both assays detected production of IFN-GAMMA- γ in co-cultures containing as low as 1% TpM.

Identification of CTL target antigens

20 **Tp1 Identification**

A CD8⁺ polyclonal T cell line from Friesian bull BV115 was generated and maintained using an HD6 expressing 4229 TpM (4229 TpM). This CTL line, termed BV115 (4229 TpM) CD8⁺ polyclonal CTL line, lysed both autologous TpM and 4229 TpM showing that the line included schizont specific HD6 restricted CTL.

25 This CTL line was used to screen the 1000 pools of 50 schizont cDNA (B & C series) following co-transfection of COS-7 cells with schizont cDNA pools and a pcDNA3 construct expressing the full length cDNA for HD6. The CTL line responded to 10 cDNA pools and the results of screening pools B1 – B200 are shown in Figure 2. Six of the ten putative positive pools were subjected to resolution and by way of illustration the results of screening the 48 resolved
30 pools from the putative positive pool B162 are shown in Figure 3. The 3-way matrix was decoded and the single cDNA were screened, the results from screening the single cDNA originating from pool B162 are shown in Figure 4. Of the five single cDNA only three were recognised by the CTL

line, all five cDNA were sequenced and found that the positive cDNA were identical whilst the negative cDNA were unrelated. It is likely that the negative cDNA were contaminated with the positive cDNA during propagation of the *E. coli* in microtitre plates since they were always grown in wells adjacent to wells containing the positive cDNA.

5 The response to the other resolved cDNA pools were due to this same cDNA, which was termed Tp1. Specific PCR primers were designed and the remaining putative positive pools were found to be positive for Tp1 cDNA. HD6 restriction recognition of Tp1 was assessed by co-transfection of Tp1 with HD6 or another BoLA class I cDNA, KN104 or transfection of Tp1 alone, Figure 5 shows that only when COS-7 cells were co-transfected with HD6 and Tp1 did the CTL
10 secrete IFN- γ . The ability of autologous immortalised skin fibroblasts to present Tp1 was assessed by transfection and compared to co-transfected COS-7 cells. Figure 6 shows that immortalised skin fibroblasts presented Tp1 to the CTL although the response was less than induced by the COS-7 cells, probably due to the reduced transfection efficiency of skin fibroblasts. Recognition of Tp1 transfected COS-7 cells and immortalised skin fibroblasts was also confirmed by the use of the
15 IFN- γ bioassay (Figure 7).

 The ability of BV115 (4229 TpM) CD8 polyclonal CTL line to lyse Tp1 transfected targets was then assessed using a ⁵¹Chromium release assay. COS-7 cells co-transfected with HD6 and Tp1, and Tp1 transfected autologous iSF were labelled and used as target cells. CTL efficiently lysed 4229 TpM and Tp1 transfected cells (Figure 8). The lysis of Tp1 expressing
20 targets was inhibited by the presence of a blocking monoclonal antibody against BoLA class I. The CTL did not lyse cells transfected with the irrelevant *T. parva* antigen PIM.

Mapping of the HD6 restricted Tp1, Tp4, Tp5, Tp7, and Tp8 CTL epitopes

 Following Exonuclease III digestion, six plasmids containing Tp1 inserts of differing sizes (Tp1 Del1 to Del6; denoted as SEQ ID NO: 6, 7, 32,33, 34, and 35 in Figure 9.), were co-
25 transfected with HD6 into COS-7 cells and recognition of plasmid clones by BV115 (4229 TpM) CD8 polyclonal CTL line assessed by IFN-GAMMA- γ ELISpot. Positive ELISpot responses were observed against clones Tp1 Del1 (SEQ ID. NO: 6) and Tp1 Del2 (SEQ ID NO:7). Both ELISpot positive and negative plasmid clones were sequenced and compared. Figure 9 shows a comparison of the predicted amino acid sequence of Tp1 (SEQ ID NO;1) with the deleted clones (SEQ ID NO:
30 SEQ ID NO: 6, 7, 32, 33, 34, and 35). The sequence comparison located the HD6 restricted CTL epitope within a 101 amino acid fragment of Tp1.

Oligonucleotide primers were generated and used in PCR to clone a 600bp fragment of Tp1, overlapping the epitope-encoding region (Tp1.6; SEQ ID NO: 40). IFN-GAMMA γ ELISpot confirmed CTL recognition of this portion of Tp1 and small overlapping fragments (Tp1.1-Tp1.5; SEQ ID NO: 35 through SEQ ID NO:40) of the 600 bp region were cloned into the mammalian expression plasmid vector pTargetT. Clones were then analysed by ELISpot and the CTL epitope was further narrowed down to a 200 bp DNA fragment corresponding to 66 amino acids (Figure 10). A cleaved PepSet library of 28 overlapping peptides each were synthesised to encompass the 66 amino acids encoded by the Tp1.2 insert (Mimotopes). Recognition of Tp1 peptides was assessed by IFN-GAMMA γ ELISpot, using autologous immortalised skin fibroblasts or murine mastocytoma P815 cells (ATCC #TIB-64, ATCC, Manassas, VA USA) stably expressing HD6 as antigen-presenting cells. Figure 11 shows the results of screening the cleaved Tp1 Pepset with BV115 (4229 TpM) CD8 polyclonal CTL line and BV115 CTL clones. The recognition of peptides #10 and #11 suggested that the epitope fell within the region RCVGYPKVKEEMLE (extending from amino acid #212 to amino acid #225 of SEQ ID NO: 1). All possible 9, 10 and 11mers were then synthesised for this sequence and screened against the polyclonal line and clones. Figure 12 shows the responses of two BV115 CTL clones to individual Tp1 peptides. Both clones responded to peptide #24, the 11mer VGYPKVKEEML (SEQ ID NO:9 and corresponding nucleotide sequence SEQ ID NO:23), suggesting that this was the minimal length HD6 restricted epitope of Tp1. This data was supported by ⁵¹Chromium release assays that demonstrated significant CTL lysis of Tp1 peptide #24 pulsed iSF or P815-HD6.

Additional experiments, using a set of 4 overlapping peptides, including the 11-mer representing SEQ ID NO:9; a 10-mer that was missing the last right-hand amino acid (amino acid number 224 of SEQ ID NO:1); a 10-mer, missing the first left-hand amino acid of SEQ ID NO:14 (amino acid number 214 of SEQ ID NO:1); and an 11-mer that included the additional left-hand amino acid (amino acid number 213 of SEQ ID NO:1) but missing that last right-hand amino acid of SEQ ID NO:14 (amino acid number 224 of SEQ ID NO:1), indicated that the minimal length of the CTL-stimulatory epitope is represented by SEQ ID NO:14.

The same types of experiments were conducted with subsets of the antigens Tp4 (SEQ ID NO:2), Tp5 (SEQ ID NO:3), Tp7 (SEQ ID NO:4), and Tp8 (SEQ ID NO:5). Within Tp4, the minimum epitope is the sequence identified by the amino acid SEQ ID NO: 14. This was established by testing a set of 8 peptides that included 9-mer polypeptide, SEQ ID NO: 14 (amino acid numbers 338 to 346 in SEQ ID NO:2), an 8-mer polypeptide representing amino acids

numbers 339 to 346 of SEQ ID NO:2, an 8-mer polypeptide representing the amino acid numbers 441 to 348 of SEQ ID NO:2; an 8-mer polypeptide representing the a peptide of amino acid numbers 338 to 345 of SEQ ID NO:2; a 9-mer polypeptide of amino acids representing amino acid numbers 339 to 348 of SEQ ID NO:2; a 10-mer polypeptide of amino acids representing amino acid numbers 338 to 347 of SEQ ID NO:2, a 9-mer polypeptide of amino acids representing amino acid numbers 339 to 347 of SEQ ID NO:2, and an 11-mer polypeptide of amino acids numbers 338 to 348 of SEQ ID NO:2. (The corresponding nucleotide sequence for SEQ ID NO:14 was determined to be the sequence represented in SEQ ID NO:28). Experiments determining the minimal length of the Tp5 that would stimulate CTLs were designed to test a set of 5 overlapping peptides in the region of SEQ ID NO: 15. These 5 peptides included the 11-mer polypeptide of SEQ ID NO:15 (amino acids numbers 8 to 95 of SEQ ID NO: 3); an 11-mer polypeptide of amino acids numbers 85 to 95 of SEQ ID NO:3 ; an 11-mer polypeptide of amino acid numbers 87 to 97 of SEQ ID NO:3; and an 8-mer polypeptide of amino acids numbers 88 to 95 of SEQ ID NO:3. The minimum Tp7 epitope is represented by the polypeptide of SEQ ID NO: 16 (and corresponding nucleotide sequence of SEQ ID NO:30). This was determined with an overlapping set of 7 polypeptides including SEQ ID NO:16 (amino acid numbers 206 to 214 in SEQ ID NO:4); an 11-mer polypeptide (amino acid numbers 204 to 214 of SEQ ID NO:4); a 10-mer polypeptide (amino acid numbers 205 to 213 of SEQ ID NO:4); a 9-mer polypeptide (amino acid number 204 to 212 of SEQ ID NO:4); an 8-mer polypeptide (amino acid numbers 204 to 211 of SEQ ID NO:4); and an 8-mer poly peptide (amino acid numbers 207 to 214 of SEQ ID NO:4). Within Tp8, the minimum epitope is represented by the polypeptide of SEQ ID NO: 17 (and corresponding nucleotide sequence of SEQ ID NO:30). This was determined by using a set of 4 overlapping polypeptides including SE ID NO:17 (amino acid numbers 269 to 277 with SEQ ID NO:5); a 9-mer polypeptide (amino acid numbers 270 to 278 of SEQ ID NO:5); a 10-mer polypeptide (amino acid numbers 268 to 277 of SEQ ID NO:5), and an 11-mer polypeptide (amino acid numbers 268 to 278 of SEQ ID NO:5).

<i>T. parva</i> antigenic polypeptides	CTL (antigen)epitopes	
	aa sequence	DNA sequence
Tp1 (SEQ ID NO: 1)	SEQ. ID. NO:9 VGYPKVKEEML	SEQ. ID. NO:23 GTAGGGTATCCAAAGGTTAAAGAAGAAATGCTA
Tp4 (SEQ ID NO: 2)	SEQ. ID. NO:14 TGASIQTTL	SEQ. ID. NO:28 ACTGGTGCTTCTATTCAAACCACTCTC
Tp5 (SEQ ID NO: 3)	SEQ. ID. NO:15 SKADVIKY	SEQ. ID. NO:29 AGCAAGGCTGACGTGATCGCAAAGTAC
Tp7 (SEQ ID NO: 4)	SEQ. ID. NO:16 EFISFPISL	SEQ. ID. NO:30 GAGTTCATTTCAATCCCAATCTCGCTC
Tp8 (SEQ ID NO: 5)	SEQ. ID. NO:17 -CGAELNHFL	SEQ. ID. NO:31 TGCGGTGCTGAATTGAACCACTTCTTG

Table 4

5 Tp1 was cloned from the Marikebuni stock of *T. parva*. The deduced amino acid sequence was compared to that of Tp1 from the Muguga stock and found to be 95.8% identical (Figure 13). The ability of CTL to recognise the Marikabuni and Muguga Tp1 was assessed using the ELISpot. BV115 (4229 TpM) CD8 polyclonal CTL line only recognised the Muguga Tp1. This is explained by a double amino acid substitution at the C-terminus of the predicted HD6 restricted epitope.

10 Evidence that Tp1 is recognised by CD8⁺ T cells from an immune resolving a challenge infection

Bull BV115, whose CTL had recognised Tp1, was challenged with a lethal dose of *T. parva* (Muguga) sporozoites and the response of purified CD8⁺ T cells to the HD6 restricted Tp1 epitope or control Tp1 peptide which did not contain any previously identified epitopes were measured longitudinally. The animal was solidly resistant to challenge with no fever or detectable parasitosis. From day 8 post-challenge, CD8⁺ T cells responded specifically to the Tp1 epitope and were sustained over the period of observation (Fig 14). The kinetics of this response is comparable to that previously described for schizont-specific CTL precursors in blood following challenge of immune cattle with *T. parva* sporozoites (McKeever *et al* 1994). Attempts were made to detect Tp1 and TpM specific lytic responses directly in peripheral blood post-challenge but these failed. An experiment was instigated to first expand schizont specific CTL numbers by a single *in vitro* stimulation with TpM and then to assess Tp1 specific lysis. Stimulated cells exhibited high cytotoxic activity against both TpM and T cell blasts pulsed with the Tp1 epitope. These data

suggest that a component of the protective CD8⁺ T cell response is Tp1-specific highlighting the potential of this antigen as a vaccine candidate.

Identification of other CTL target antigens

Four other CTL target antigens, namely Tp4, Tp5, Tp7 and Tp8, have been identified through screening and resolution of the schizont cDNA library using either the ELISpot assay or bioassay. These assays utilised CTLs generated from five cattle representing four class I MHC genotypes. Cells transfected with these four antigens were recognised and lysed specifically by CTLs. Further assays have been performed to define the CTL epitope in Tp5. Experiments have been carried out which demonstrate that Tp5 is recognised by *ex vivo* CD8⁺ T cells obtained from an immune animal (BV050). These results are summarised in Table 5.

Antigen	CTL	Assay for ID	Lysis	Epitope	Ex vivo response
Tp4	BV057 BX063 BX065	ELISpot Bioassay	✓	Not done	Not done
Tp5	BV050	ELISpot	✓	✓	✓
Tp7	BW012	ELISpot	✓	Not done	Not done
Tp8	BX063 BX065	ELISpot	✓	Not done	Not done

Table 5: A summary of results showing the identification of further CTL target antigens.

Nucleotide and deduced amino acid sequences and putative identity of the 5 candidate antigens

Following confirmation of the candidates as CTL target antigens, the individual cDNA were sequenced and confirmed to be of *T. parva* origin by interrogating the *T. parva* genome sequence database. BLAST searches (Altschul *et al* 1990) of DNA and protein databases were performed and homologues of some of the antigens identified. SignalP (Nielsen *et al* 1997) and Tmpred (http://www.ch.embnet.org/software/TMPRED_form.html) analyses were conducted to

predict the presence of a signal peptide and transmembrane domain. SEQ ID NO: 17-22 indicate the DNA and SEQ ID NO: 1-5, the deduced protein sequences of the five candidate antigens.

Protein Expression

Construction of Plasmids

5 The reading frames of *T. parva* candidate antigen genes were amplified by PCR using Taq polymerase (Promega, Madison, WI USA 53711) from the original full-length genes in their respective plasmids in pcDNA3. Both the forward and reverse primers contained restriction enzyme sites (Table 6). The PCR products were digested with the respective restriction enzymes, and ligated into bacterial His-tag expression vectors, pQE30 (Qiagen, 28159 Avenue Stanford, 10 Valencia, CA91355) or PET28 (Novagen, Madison, WI 53719 USA). The plasmids were transformed into *E. coli* strain DH5 α (Life Technologies, Carlsbad, CA 92008, USA). All the plasmids were sequenced to ensure that they harbored no substitutions compared to the original genes. Purified plasmids were then used to transform competent BL21 DE3 bacterial cells.

Gene (Plasmid)	Forward Primer (Restriction Site)	Reverse Primer (Restriction Site)	Expression Vector	PCR Product(s) (kb)
Tp1 (pcDNA3)	GGATCCCCGGAAGAAAG AGGAACTC (<i>Bam</i> HI) (SEQ ID NO: 33)	CTGCAGTTAAT TTTGTAGGTAAATTTG (<i>Pst</i> I) (SEQ ID NO: 37)	pQE30	1.5
Tp4 (pcDNA3)	AATGTAGTTTTATCTAAATTGCC A (<i>Bam</i> HI) (SEQ ID NO: 34)	GAGGAGATAAG TTGAGAGCAACATC (<i>Sal</i> I) (SEQ ID NO: 38)	pQE30	0.4
Tp5 (pcDNA3)	GGATCCGAAATGGCGAAAAATA AAGGCAAAGGA (<i>Bam</i> HI) (SEQ ID NO: 35)	CTGCAGTTATAAATCAT CGATATCGAAATCT (<i>Pst</i> I) (SEQ ID NO: 39)	pQE30	0.6
Tp7 (pcDNA3)	GCCAAGAATTCGATGACATCAA AGGACGAG (gene internal <i>Bam</i> HI site) (SEQ ID NO: 36)	GGCGCGGCCGCGTCAA CTTCCTCCATTTTG (<i>Not</i> I, <i>Xho</i> I) (SEQ ID NO: 40)	pET28b	2.0, 1.1

Table 6: Primers, restriction sites and vectors used for the cloning of *T. parva* antigens for protein production.

Expression of the proteins

Single BL21 DE3 bacterial colonies bearing the recombinant plasmids were isolated and
 5 cultured in 2XYT (formula) at 37°C to an OD₆₀₀ of 0.6, and protein expression induced by addition
 of IPTG to a final concentration of 1mM, and further cultured for 4 h. The cells were harvested by
 centrifugation at 4000 g for 20 min. Recombinant proteins were isolated by either the native or
 denaturing nickel-nitrilotriacetic (Ni-NTA) agarose according to the manufacturer's protocol
 (Qiagen, 28159 Avenue Stanford, Valencia, CA91355), dialyzed against PBS and stored at -20 °C.
 10 Purified proteins were checked on 12% SDS-PAGE gels and Western blot. Protein concentration
 was determined by the BCA Protein Assay reagent (PIERCE, Rockford, IL 61105, USA). Bacterial
 cells or purified proteins were applied to a 12% SDS-PAGE gel under denaturing conditions.
 Proteins were electroblotted onto nitrocellulose sheets (Schleicher and Schull, Dassel, Germany).
 Mouse His-tag antibody (SIGMA) was used as the primary antibody, while anti mouse horse-
 15 raddish peroxidase conjugate (SIGMA) was used as the secondary antibody followed detection
 with 3,3'-Diaminobenzidine and hydrogen peroxide.

The reading frame of the segments Tp1, Tp4 and Tp5 amplified and cloned into the
 bacterial expression vectors harbored no substitutions compared to the original gene sequences.
 Recombinant protein containing His-tag were produced from all the constructs (Figure 15), and all
 20 can be determined by immunoblotting using His-tag antibody.

Polymorphism in CTL target antigens

Specific Tp1 forward (IL #12588: 5'-ATG GCC ACT TCA ATT GCA TTT GCC-3'
 (SEQ ID NO: 41) and reverse (IL #12589: 5'-TTA AAT GAA ATA TTT ATG AGC TTC-3')
 (SEQ ID NO: 42) primers were designed and used in PCR to amplify a 430 bp region containing
 25 the BV115 CTL epitope from genomic DNA of *T. parva* (Kakuzi521, Kilifi KL2, Kilifi KL1,
 Kilifi BR305, Nyairo IL02, Nyairo IL17, D409 Tp Mariakani, Buffalo7344cl, Zambia 2 and
 Uganda) isolated from infected animals in different regions. PCR products were sequenced and
 their deduced amino acid sequences were compared with Tp1 (Figure 17). The result showed
 variations among the Tp1 studied. This strongly indicated that Tp1 is polymorphic.

30 Vaccination strategy

Cattle trials are performed to assess the vaccine potential of identified CTL target
 antigens utilizing a recombinant canarypox virus (patented by Merial Ltd) as an antigen delivery

method. The first of these trials is testing one of the candidate antigens and involves use of 16 cattle. Animals are inoculated intramuscularly with 1 ml of vaccine (1×10^8 pfu of virus) and boosted similarly after 4 weeks. Following a further 4 weeks, cattle are subjected to an LD₁₀₀ challenge with *T. parva* sporozoites by administering subcutaneously 1 ml of diluted stablited infective material. Animals are monitored parasitologically and clinically over a period of 2-3 weeks to determine whether the vaccine has protected. It is expected that the vaccines are protective.

Immunological assays are performed following immunization and challenge to evaluate antigen-specific CTL responses and relate these to the outcome to challenge.

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All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following outline of the invention ("claims").

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